



MEI...S AND COMPOSITIONS FOR INCREASING
ANTIBODY PRODUCTION

Reilly et al. Attorney Docket P1957R1

Sheet 4 of 33

1 GAATTCACCT TCTCCATACCT TTGGATAAGG AATATACACAG ATGAAAAATC TCATTCTGTA GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAGTTGA AGAGGTATGA AACCTATATCC TTATATGCTG TACTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTTCT TCTCAGCTTA

101 GAACGTGTG CGCAGGTAGA AGCTTTGGAG ATTATGTCFA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGAATTGAT CAGGTAGAGG
CTTGACACAC GGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGGTTTTTAC TGGTTGTGCG CAACATACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACATAGG GAGCTGCTGC GCGATTAGCT AAAGAAGTTA TTGAAGCATC CTCGTACGTA
CCCCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGAGCAG CGGTAATGCA TTTCTTCAAT AACTTCTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCATRA AGTTGTCACG GCGAGACTT ATAGTGGCTT TGTTTTATT TTTTAATGTA TTGTAACTA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATTAAT AAACATTGAT CATGCGTTCA

401 TCAGTAAAA AGGGTATCTA GAATTATGAA GAAAAACATC GCTTTCTTC TTGCACTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
AGTGCATTTT TCCCATAGAT CTTAATACCT CTTTGTGTAG CGAAAGAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTGTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^start STII signal TIR-2 start light chain^

501 CAGATGACCC AGTCCCGAG CTCCCTGTCC GCTCTGTGG GCGATAGGCT CACCATCACC TCAGAGCCA GTCCGACAT CAAGAGCTAT CTGAACCTGT
GTCTACTGGG TCAGGGGCTC GAGGACAGG CGGAGACACC CGCTATCCCA GTGTGTAGG AGCTCTGGT CAGGCTGTA GTTCTGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTA CTATGCTACT AGTCTGCTG AGAGTCCC TTCTGCTTC TCTGATCG GTTCTGGGAC
TAGTTGCTT TGGTCTTTT CGAGGCTTTC ATGACTAAT GATACGATGA TCAGAGCAC TTCTCAGGG AAGAGCGAAG AGACCTAGG CAAGACCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G T

701 GGATTACACT CTGACCATCA GCAGCTGCA GCCAGAGAC TTCCGCACTT ATTACTGTCT TCAGCAGGA GAGTCTCCAT GGACATTGG ACAGGTTACC
CCTAATGTGA GACTGGTAGT CGTCAGAGCT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCTGCTT CTCAGAGGTA CCTGTAAACC TGTCCEATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

801 AAGGTGAGA TCAACGAC TCCTGCTGCA CCATCTGTCT TCATCTTCCC GCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTCTGCTGCG
TTCCACCTCT AGTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGG CGGTAGACTA CTGTCACCT TTAGACCTTG ACAGAGACAA CACACGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCGAGA GAGGCCAAG TACAGTGAA GTTGATAAC GCCTCCCAT CGGTTAATC CCAGGAGT GTACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGAGGTTA GCCCATGAG GTTCTCTCA CAGTGTCTCG TCTGTCTGTT

160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GAGCTGAGC AAAGCAGCT ACAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCTGAGC
CCTGTCGTGG ATCTCGAGT CGTCGNGGA CTGCGACTCG TTTGCTGTA TGTCTTTGT GTTTCAGATG CGGAGCTTC AGTGGTAGT CCCGACTCG

193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

FIG. 2A

DS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

Reilly et al. Attorney Docket P1957R1

Sheet 5 of 33

1001 GGAGCGACC TACAGCGTCA GCAGCAGCTT GACGCTGAGC AAGCAGACT ACAGAGACT CAAAGTCTAC GCGGCGAAG TCACCCATGA GGGCCCTGAGC
 193 ~~CGCTGCTGG ATGTCGGAGT CGTGGGGA CTGCGACTGG TTTCGCTGA TGCTCTGT GTTCAGATG GCGAGCTTC AGTGGAGT CCCGACTCG~~
 D S T P S L S S T L T M S K A D Y E K H K V Y A C E V H Q S L S
 1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGA GAGTGTAAAT TAAACCTCT AGSCCGGACG CATCGTGGG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
 AGCGGGCAGT GTTCTCGAA GTTGCCCT CTCAATA ATTTAGGAGA TCGGGCTGC GTAGCACGC TCGAGCCATG GSCCCCTAGA TCGGATTC
 226 S P V T K S F N R G E C O
 1201 CTCGTTGCC GCGGGGCTT TTTATTGTT GCGACGCGC ATCTGAATG AACTGTGTG GCAGGTAGAA GCTTTGGAGA TTATGTCAC TGCATGCTT
 GAGCAACCG CGGCCGCAA AAATAACAA CGGCTGGCG TAGACTTAC TTGACACAG CGTCCATCTT CGAACCTCT ATAGCAGTG AGTTACGAA
 1301 CGCAATATG CGCAATATG CCAACAGCG TTGATTGATC AGTGAAGG GCGCTGTAC GAGTAAGC CCGATGCCAG CATTCCTGAC GACGATACGG
 GCGTTATACC GCGTTTACT GGTTCGCC AACTAATAG TCCATCTCC CCGGACATG CTCATTTCC GGTACGGTC GTAAGGACTG CTGCTATGCC
 1401 AGCTGCTGG CGATTACGTA AAGAGTTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTCACACG CTGTCTAATA GTTGTACGG CCGAGACTTA
 TCGACGAGCG GCTAATGCAT TTCTCAATA ACTTCGTAG AGCATCAT TTTCATTTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGTCTGAT
 1501 TAGTGGCTT GTTTTATTT TTTAATGTA TTGTAATAG TACGCAAGT CACGTAATAA GGTATCTAG AATTATGAG AAAACATCG CTTTCTTCT
 ATCAGCGAA CAAAATAAA AATTACATA AACATTGATC ATGCTTCAA GTGCATTTT CCATAGATC TTATATCTT TTTTGTAGC GAAAGAAGA
 M K K N I A F L L
 ^start still signal TIR-2
 1601 TGCATCTATG TTCGTTTTT CTATTGCTAC AAACGGTAC GCTGAGTTC AGTGTGGA GTCTGGGT GCGCTGGTGC AGCCAGGGG CTCACTCCGT
 ACGTAGATAC AAGCAAAAG GATAACGATG TTGCGCATG CGACTCAAG TCGACCACT CAGACGCCA CCGGACCAAG TCGTCCCGG GAGTGAGGCA
 10 A S M F V F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R
 ^start heavy chain
 1701 TTGCTCTG GACCTCTG CTTCAATATT AAGGATCT ACATGACTG GTCTGCTAG GCGCCGGTA AGGCGCTGA ATGGTGA TTGATGATC
 AACAGGACAC GTCGAAGACC GAAGTTATA TTCTCATGA TGTACGTGAC CCAGGCGATC GCGGCGCAT TCCCGGACT TACCCAACT AACTAATAG
 43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P
 1801 CAGAGCAAG CAACAGATC TATGACCGA AGTTCAGGA CCGTGCACT ATAGCGCTG ACAATCCAA AAACACAGCA TACCTGCAGA TGAACAGCTT
 GTCTCGTCC GTTGTGCTAG ATACTGGCT TCAAGTCTT GGCACGCTG TATTGCGAC TGTAAAGTT TTTGTGCT ATGGAGTCT ACTTGTGGA
 77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L
 1901 GCGTCTGAG GACACTGCCG TCTATTATTG TGCTGAGAC AGGCGCTT ACTTGACTA CTGGGTCAA GGAACCTGG TCACGCTC CTCGGCTCC
 CGCAGACTC CTGTGACGGC AGATAATAAC ACAGCTCTG TCGCGCGAA TGAAGTGTAT GACCCAGTT CTTGGGACC AGTGGCAGAG GAGCCGGAGG
 110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S
 2001 ACCAAGGCC CATCGTCTT CCCCCTGCA CCTCTCCA AGAGCACCTC TGGGGGACA GCGGCCCTGG GCTGCTGT CAAGGACTAC TTCCCCGAAC
 TGGTTCCCG GTAGCCAGAA GGGGACCGT GGGAGAGGT TCTCTGGAG ACCCCGCT GCGCGGACC CGACGACCA GTTCTGTAG AAGGGCTTG
 143 T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P
 2101 CGGTACGCT TCAAGGCCC TGACGAGCG GGTGCACACC TTCCGCGCTG TCCTACAGTC CTCAGACTC TACTCCCTCA GCAGCGTGT
 GCCACTGCCA CAGCACCTTG AGTCCGCGG ACTGTGCTCC GCACGTGTG AAGGGCGAC AGGATGTCAG GAGTCTGAG ATGAGGAGT CGTGACCA
 177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V

FIG. 2B

METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

Reilly et al. Attorney Docket P1957R1
Sheet 6 of 33

2101 CGGTGAAGGT GTCTGGAGC TCAGGCGCC TGACGAGCGG CGTGCACACC TTCCCGGCTG TCTTACAGTC CTAGAGACTG TACTCCCTCA GCAGCGTGGT
GCCAGTGCCA CAGCACTCTG AGTCGGGCGG ACTGGTGGCG GCACGTGGG AAGGCGGAC AGGATGTGAG GAGTCTGTAG ATGAGGAGGT GTCTGACCCA
177 V T V S W N S A L T S G V H T P P A V L Q S S G L Y S L S S V V
2201 GACTGTGCC TCTAGCAGCT TGGGCACCCA GACTTACATC TGCAAGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA AGAAGTTGA GCCCAATCT
CTGACACGGG AGATCGTGA ACCCGTGGGT CTGGATGTAG ACGTTCACAT TAGTGTGG GTCTGTGG TTCCACTGT TCTTCACT CGGTTTGA
210 T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S
2301 TGTGACAAA CTCACACATG CCCACCGTGC CCAGCACTG AACTCTGG GGGACGCTCA GTCTTCTCT TCCGCCAAA ACCCAAGGAC ACCCTCATGA
ACACTGTTTT GAGTGTGTAC GGTGGGACG GGTGTGTAC TTAGAGACCC CCTTGGAGT CAGAAAGAGA AGGGGGTTT TGGTTCTG TGGGAGTACT
243 C D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I
2401 TCTCCCGAC CCTGAGGTC ACATGCTGG TGGTGGAGT GAGGCAGAA GACCTGAGG TCAAGTTCAA CTGTACGTG GACGGCGTGG AGGTGCATAA
AGAGGGCTG GGGACTCCAG TGTAGCCACC ACCACTGCA CTGGTGCTT CTGGGACTCC AGTTCAGTT GACCATGCAC CTGCCGACCC TCCAGGTATT
277 S R T P E V T C V V D V S H E D P E V K F N W Y V D G V E V H N
2501 TGCCAAGACA AAGCCGCGG AGGACAGTA CAACGACG TACCGTGG TACGCTCTCT CACCGTCTG CACCAAGACT GGCTGAATGG CAAGGAGTAC
ACGGTTCTGT TCGGCGCCC TCCTGCTCAT GTGTGCTGC ATGCACACC AGTCGACGA GTGGCTCTGA CGACTTACC GTTCTCTATG
310 A K T K P R E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y
2601 AAGTGAAGG TCTCCAAACA AGCCCTCCA GCGCCCATCG AGAAACCAT CTCCAAGCC AAAGGGGAGC CCGGAGAAC ACAGGTGTAC ACCTGCCCC
TTACAGTTCC AGAGTTGTT TCGGGAGGT CGGGGTAGC TCTTTGTA GAGTTTGG TTTCCTCTG GGGCTCTTGG TGTCCACATG TGGGACGGG
343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P
2701 CATCCCGGA AGAGATGACC AAGAACCAGG TCAGCTGTC CTGCTGTC AAAGCTTCT ATCCAGCA CATCCCGTG GAGTGGAGA GCAATGGGA
GTAGGGCTCT TCTCTACTG TTCTTGTCC AGTCGACTG GACGGACCAG TTTCGAAGA TAGGTCCT GTAGGGCAC CTCACCTCT CGTTACCCGT
377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q
2801 GCGGAGAAC AACTACAAGA CCAGCCTCC CGTGTGAC TCCGACGCT CCTTCTCTCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
CGGCTCTTG TTGATGTTCT GTTGGGAGG GCACGACCTG AGGTGCGGA GGAAGAAGA GATGCTTTC GAGTGGCACC TGTTCGTGTC CACGTCGTC
410 P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q
2901 GGGACGTCT TCTCATGCTC CGTATGTCAT GAGGCTCTGC ACAACACTA CAGCAGAAAG AGCTCTTCCC TGTCTCGGG TAAATTAAGA TGCACGGCC
CCCTTGACA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTGTGTAT GTGCTCTTC TGGGAGGG ACAGAGGCC ATTTATTCGT ACGTGGCGG
443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O
3001 CTAGAGTCCC TAACGCTCGG TTGCGCGCGG CGGTTTTTA TTGTTAACTC ATGTTGACA GCTTATCATC GATAAGCTTT AATGCGTAG TTTATCACAG
GATCTCAGG ATTGCGAGCC AACGCGCGCC CGCAAAAAT AACAAATTGAG TACAACCTGT CGAATAGTAG CTATTCGAAA TTACGCCATC AATAGTGTG
3101 TTAATTTGCT AACGCAGTCA GGCACCGTGT ATGAATCTA ACATGCGCT CATGTCATC CTCGGCACC TCACCTGGA TGTGTAGGC ATAGGCTTGG
AATTTAACGA TTGGTCACT CCGTGGCACA TACTTAGAT TGTACGGA GTAGCAGTAG GAGCCGTGGC AGTGGACCT AGACATCCG TATCCGAACC
3201 TTATGCGGT ACTGCGGGC CTCTTGGGG ATATGTCOA TT
AATACGCCA TGACGCGCG GAGAACGCC TATAGAGGT AA

FIG. 2C

1 GAATTCAACT TCTCCATCT TTGGATAAG AATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTT AAGCTTGCCC AAAAAGAGA AGAGTCGAAT
CITTAAGTTGA AGAGGTATGA AACCTATTCC TTATGCTG TACTTTTAG AGTAACGACT CAACATATAA TTGCAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CITGACACAC GGTCCATCT TCGAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGGTTTATC TGGTTGTGCG CAACATACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCGGATGCCA GCATTCCTGA CGAGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTACAGTA
CCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGAGCAGC CGCTAATGCA TTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCTATAA AGTTGTCACG GCGGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAATGTA TTGTAACTA GTACGCAAGT
TTTTCATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAGA AGGGTATCTA GAATTATGAA GAAGATATC GCATTTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAACGCTA CGCTGATATC
AGTGCAATTT TCCGATAGAT CTTAATAGTT CTTCTATAG CTTAAGAGAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^STII signal TIR -1 ^Light chain

501 CAGTTGACCC AGTCCCGAG CTCCTGTCC GCCTGTGCG GCGATAGGT CACATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAACCTGGT
GTCAACTGGG TCAGGGGCTC GAGGGACAGG CCGTATCCCA GTGCTAGTGG AGTCCGCTT CAGTCCTATA ATCGTGTATA AATTGACCA

26 Q L T Q S P S L S A S V G D R V T I T C S A S Q D I S N Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTTCACTCC CTTCTCCACT CTGAGTCCC TTCTGCTTC TCTGATCCG GTTCTGGGAC
TAGTTGCTT TGGTCTTTT CGAGGCTTTC ATGACTAAT GAAGTGGAG AGAGAGTGA GACCTCAGG AAGACGAG AGACCTAGG CAAGACCCCTG

60 Q Q K P G K A P K V L I Y F T S S L H S G V P S R F S G S G S T

701 GGAATTCAC CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGCA ACAGTATAGC ACCGTGCGGT GGACGTTGG ACAGGTTACC
CCTAAAGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGT TGTATATCG TGGCACGCA CCTGCAAAACC TGTCCCATGG

93 D F T L T I S S L Q P E D F A T Y Y C Q Q Y S T V P W T F G Q G T

801 AAGGTGGAGA TCAACGAAAC TGTGCTGCA CCACTGTCT TCACTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC
TTCCACCTCT AGTTTGCTG ACACCGACGT GGTAGACAGA AGTAGAAGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CAGACGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCAGA GAGGCCAAG TACAGTGGAA GGTGGATAAC GGCCTCAAT CGGTTAATCT CCAGGAGAGT GTACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGTTTC ATGTCACCTT CCACCTATTG CCGGAGTTA GCCATTGAG GGTCTCTCTA CAGTGTCTCG TCTGTGCTT

160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GAGCAGCACC TACAGCCTCA GCAGCACCTT GAGCCTGAGC AAGCAGACT ACGAGAACA CAAAGTCTAC GCTGCEAAG TCACCCATCA GGGCCTGAGC
CCTGCTGGG ATGTCGAGT CGTCTGGGA CTGCGACTCG TTGCTCTGA TGTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCGGACTCG

193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

FIG. 4A

ODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

Reilly et al. Attorney Docket P1957R1

Sheet 11 of 33

1001 GGACACACAC TACAGCCTTA GCAGACCCG GACGCTGAGC AGGCGAGACT ACAGAAACA CAAGAGTAC GCCTGCGAGC TACCCACATC GGGCCTGAGC
 193 CCGCTGCTGG ATGTGAGT CCGCAGGGA CTGCGAGTGG TTCTGCTGTA TCTCTTTGT GTTTCAGATG CCGAGGCTTC AGTGGTAGT CCGGACTCG
 1101 TCGCCCTCA CAAGAGCTT CAACAGGGA GAGTCTTAAT TAAATCTCT AGCGGAGC CATCTGGG AGCTCGGTAC CCGGGATCT AGGCTAAGC
 226 S P V T K S F N R G E C O
 1201 CTCGTTGCC GCGGGCGTT TTTTATGTT GCGAGCGGC ATCTGAATG AACTGTGC GCAGTAGAA GCTTTGAGA TTATGTCAC TGAATGCTT
 GAGCCACGG CCGCCCGCAA AAAATACAA CCGCTGCGG TAGAGTTAC TTGACACAG CGTCCATCTT GGAACCTCT AATAGCAGT ACCTACGAA
 1301 CGCATATGG CGCAAAATGA CCAACAGGG TTGATTAATC AGGTAGAGG GCGCTGTAC GAGTAAAGC CGATGCCAG CATTCCTGAC GACGATACGG
 GCGTTATACC GCGTTTACT GGTGTGCGC AACTAATAG TCCATCTCC CCGGACATG CTCCATTTG GGTACGGTC GTAGGAGTGT CTGCTATGCC
 1401 AGTCTCTGG CGATTAGCTA AAGAATTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTTCAACG CTGTCAATAA GTTGTACGG CCGAGACTTA
 TCGAGGACG GCTAATGCAT TTCTCAATA ACTTGTAGG AGCATCAT TTCTAATTAG AAAAGTTGTC GACAGTATT CAACAGTGCC GGTCTGAAT
 1501 TAGTCGCTTT GTTTTATTT TTTAATGAT TTGTAATAG TACGCAAGT CACGTAATAA GGTATCTAG AATTANGAG AAGAATATCG CATTTCTTCT
 ATCAGCGAAA CAAAATATA AATATACATA AACATTGATC ATGGTTCAA GTGCTATTTT CCGATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
 1 M K K N I A F L L
 ^STII Signal TIR-1
 1601 TGATCTATG TTGTTTCTT CTATGCTAC AAACGGTAC GCTGAGTTC AGTGTGGA GTCTGGGT GGTCTGTGTC AGCCAGGGG CTCATCCCT
 ACCTAGATAC AAGCAAAA GATAAGATG TTGCGCAT GCACTCAAG TCGACCAT CAGACGCCA CCGGACCAAG TCGTCCCCC GAGTGAGGA
 10 A S M F V F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R
 ^start heavy chain
 1701 TGTCTCTGG CAGCTTCTGG CTATACCTTC ACCACTATG GPATAACTG GTTCCTCAG GCGCGGGA AGGCTCTGGA ATGGTTGA TGGATTACA
 AACAGGACAC GTCAAGACG GATATGGAAG TGTGTATAC CATATTGAC CCAGGCAATC TGTGAGGT TCGGAGCTT TCCCGGACCT TACCAACCT ACCTAATGT
 43 L S C A A S G Y T F T N Y G I N W V R Q A P G K G L E W V G W I N T
 1801 CCTATACCG TGAACCGACC TATGCTGGG ATTTCAAGG TCGTTTCACT TTTTCTTAG ACACCTCCA AAGCAGACA TACCTGCAGA TGAACAGCT
 GGATATGCC ACTTGGCTGG ATACGAGCC TAAAGTTTGC AGCAAGTGA AAGAATC TGTGAGGT TCGTGTCTGT ATGAGCTGT ACTTGTGGA
 77 Y T G E P T Y A A D F K R R F T F S L D T S K S T A Y L Q M N S L
 1901 GCGGCTGAG GACTGTGCG TCTATTACTG TGCAGATAC CCGCACTAT ATGTGAACGA GCGGAGAGC CACTGTATT TCGAGCTGT GGTCAAGGA
 CCGGCGACT CTGTGACGC AGATAATGAC ACCTTTCTAG GCGGTGATA TACACTGT CCGCTTCTCG GTGACCATAA AGCTGCAGAC CCCAGTTCT
 110 R A E D T A V Y Y C A K Y P H Y Y V N E R K S H W Y F D V W G Q G
 2001 ACCCTGGTCA CGTCTCTC GGCCTCCAC AAGGGCCCAT CCGTCTTCC CCGTCAAGC TCTTCAAGA GCACCTCTGG GGGCAGCAGC GCGCTGGCT
 TGGACCACT GGCAGAGGAG CCGGAGTGG TTCCCGGGA GCCAAGGG GAGCGTGG AGGAGTTCT CGTGAGACC CCGTGTGCG CCGGACCGA
 143 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C
 2101 GCGTGTCAA GCACTACTTC CCGAAGCGG TGAGGTGTC GTGAATCTA GCGGCGCTGA CAGCGGCGT GCACACTTC CCGGCTGTCC TACATCTC
 CCGACCACTT CCGTATGAAG GCGTGTGCC ACTGCCAG CACTTGAAT CCGCGGACT GTTCGCGCA CGTGTGAG GCGGACAGG ATGTGAGG
 177 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S

lambda to terminator^

FIG. 4B

2101 GCTGTGCAA GGAATCTAC CCGAAGCCG TGAAGTGTG GGGGCTTCA GGCCTCTTC CAGGCGGT GGCCTGTTC TGAAGTCTC
CGGACCAATT CCTGAGGAG GGGCTTGGC ACTGACACAG CACTTGAAT CCGGGGACT GGTGCGGCA CGTGTGAG GGCACAGG ATGTCAAGG
177 L V K D Y F P E P V T V S W N S S A L T S G V H F P A V L O S S
2201 AGGACTTAC TCCCTCAGCA GCGTGTGAC TGTGCTCTT AGCAGCTTG GCACCCAGC CTACATCTG AACGTGATC ACAAGCCAG CAACACCAAG
TCCTGAGATG AGGAGTCTG CGCACCACTG ACACGGGAG TGTGCAACC CGTGGGCTG GATGTAGAG ITGCACCTAG TGTTCGGGTC GTTGTGTTT
210 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K
2301 GTGGACAGA AAGTTGAGC CAAATCTGT GACAAACTC ACATGTC CCGGACCC TGAAGTCA TGGTGTG TGAAGTCA CCGGAGTCA AGTTCAACTG
CACCTGTTCT TTCAACTCGG GTTTAGACA CTGTTTGTAG TGTGTAGG TGGACCGGT CGTGAATTT AGGACCCCTC TGGCAGTCAAG AAGGAGAAG
243 V D K K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P
2401 CCCCAGAAC CAGGACACC CTGATGATCT CCGGACCC TGAAGTCA TGGTGTG TGAAGTCA CCGGAGTCA CCGGAGTCA AGTTCAACTG
GGGTTTGG GTTCTGTGG GAGTACTAGA GGGCTGGG ACTCAGTGT AGCACCACC ACCTGCTCTG GGTGCTCTG GGTGCTCTG TCAAGTTGAC
277 P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W
2501 GTAGTGGAC GCGTGGAG TGCATATGC CAAAGCAAG CCGGCGGAG AGCAGTACA CAGCAGTAC CCGTGTG TGAAGTCA CCGGAGTCA AGTTCAACTG
CATGACCTG CCGCACCTCC AGTATTAC GTTCTGTTC GCGGCTCTC GGTGCTCTC GGTGCTCTC GGTGCTCTC GGTGCTCTC GGTGCTCTC
310 Y V D G V E V H N A K T K P R E Q Y N S T Y R V V S V L T V L H
2601 CAGGACTGC TGAATGCAA GAGTACAAG TGAAGTCT CCAAGAAC CCTCCAGC CCGGAGTCA CCGGAGTCA CCGGAGTCA AGTTCAACTG
GTCTGACCG ACTTACGTT CCTCATGTT CCGGAGTCA GGTGTTTC AGTGTGTT GGTGTTTC GGTGTTTC GGTGTTTC GGTGTTTC GGTGTTTC
343 Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R
2701 GAGAACCA GGTGTACACC CTGCCCCAT CCGGAGGAG GATGACCAAG AACGAGTCA GGTGACTG CCGTGTG TGAAGTCA CCGGAGTCA AGTTCAACTG
CTCTGTGT CCACATGTG GACGGGTA GGGCTCTCT CTACTGTTC TGTGCTCT GGTGCTCT GGTGCTCT GGTGCTCT GGTGCTCT
377 E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I
2801 CCGGCTGGAG TGGAGAGCA ATGGGAGC GAGAACCAAC TACAGACA CCGTCTCCGT GGTGACTCC GAGGCTCT TCTTCTCTA CAGCAAGCTC
GCGGCACCTC ACCCTCTGT TACCGTCTG CCTCTGTG ATGTTCTGT GCGGAGGCA CCGGAGTCA GGTGACTCC GAGGCTCT TCTTCTCTA CAGCAAGCTC
410 A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L
2901 ACCGTGGACA AGAGCAGGTG GCAGCAGGG AACGTTCT CTGCTCTGT GATGATGAG GGTGACTCA ACCACTAC GCAGAGAGC CTCTCCCTGT
TGGCACCTGT TCTGTCAC CGTCTCTCC CGTCTCTCC TGGAGAGA GTACGAGCA CTACTACTC CGAGAGTGT TGTGATGT GGTCTCTCTG GAGAGGACA
443 T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S
3001 CTCGGGTAA ATAAGCATG GACGGCCCTA GATCCCTTA CCGTCTGT GCGGAGCAAC GCGGCGGCG TTTTATTG TTAAGTATG TTTGAGAGT TATCATCAT
GAGGCCATT TATTCGTACG CTGCGGGAT CTCAGGAT GCGGAGCAAC GCGGCGGCG TTTTATTG TTAAGTATG TTTGAGAGT TATCATCAT
477 P G K O
*lambda terminator
3101 AAGCTTTAAT GCGGTAGTT ATCAGATTA AATTGCTAAC GAGTCAAGC ACCGTGTATG AATCTAACA ATGCTCTAT CGTCTCTCT GGCACCGTCA
TTGAAATTA GCGCATCAA TAGTGTCAAT TTAAGATTG CCGTCAAGT TGGACATAC TTGATTTGT TACGCGAGTA GCAGTAGGAG CCGTGGCAGT
3201 CCTGTGATG TGTAGGATA GCGTTGGTA TGGCGTACT GCGGGGCTC TTGCG
GGGACCTAC ACATCCGTAT CCGAACCAAT CCGGCCATGA CCGGCCGAG AACGC

FIG. 4C

METHODS AND COMPOSITIONS FOR INCREASING
ANTIBODY PRODUCTION

Reilly et al. Attorney Docket P1957R1
Sheet 13 of 33

3201 ~~CCCTGATGC TGTAGGCTAT GGTGTGTTA TCCCGTACT GCGGGGTC TTGCG~~
~~GGACCTACG ACATCCGAT CCGACCAAT ACGGCGATGA CCGGCGGAG AACGC~~

FIG. 4D

1 GAATTCAACT TCTCCATACT TTGGATAAGG AATATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTGGAACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GGGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTGCG CAACATACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCTATA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTTATT TTTTAAATGTA TTTGTAACATA GTACGCAAGT
TTTTCAATTA GAAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTCTTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGTA CGCTGATATC
AGTGCAATTT TCCCATAGAT CTTAATACCT CTTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
STII Signal Sequence TIR-1 Anti-Tissue Factor Light Chain

501 CAGATGACCC AGTCCCCGAG CTCCTGTGTC GCGATAGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAAGTGGT
GTCTACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S R S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCCCTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCCTCAGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCCCAACTT ATTACTGTCT TCAGCACGGA GACTCTCCAT GGACATTTGG ACAGGGTACC
CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCTT CTCAGAGGTA CCTGTAAACC TGTCCCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

FIG. 1A

801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCACTCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCAGA GAGGCCAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CCGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGGTTTC ATGTCACTT CCACCTATTG CCGGAGGTTA GCCCATTCAG GGTCTCTCA CACTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GAGCCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGGGAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTGGAGT CGTCTGGGA CTGGACTCG TTTCGCTGA TGTCTTTGT GTTTCAGATG CCGACGCTT AGTGGTAGT CCCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGAGC CATCTGGTAC CCGGGGATCT AGGCCTAAGC
AGCGGGCAGT GTTCTCGAA GTTGTCCCT CTCACAATTA ATTTAGGAGA TCGGCCCTGC GTAGCACCGC TCGAGCCATG GCGCCCTAGA TCCGGATTGC
226 S P V T X S F N R G E C O

1201 CTCGGTTGCC GCGGGCGTT TTTTATTGTT GCCGACGCG ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TCGAATGCTT
GAGCCACGG CCGCCCGCAA AAAATAACAA CCGCTGGCG TAGAGCTTAC TTGACACAG CGTCCATCTT CGAAACCTCT AATAGCAGT ACGTTACGAA

1301 CGCAATATGG CGCAAATGA CCAACAGCG TTGATTGATC AGGTAGAGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG
GCGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCCATCTCCC CCGGACATG CTCCATTTCC GGCTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACCG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAAATTAG AAAAGTTGTC GACAGTATT CAACAGTGCC GGCTCTGAAT

1501 TAGTGCCTTT GTTTTATTT TTTAATGTAT TTGTAACTAG TACGCAAGTT CACGTAAAAA GGTATCTAG AATTATGAG AAGAATATCG CATTCTCTCT
ATCAGCGAAA CAAAAATAA AAATTACATA AACATTGATC ATCGGTTCAA GTGCATTTT CCCATAGATC TTAATACTTC TTCTATAGC GTAAAGAAGA

M K K N I A F L L
^STII Signal Sequence TIR-1

FIG. 1B

1601 TGCATCTATG TTGTTTTTTT CTATTGCTAC AAACGGCTAC GCTGAGTTT AGCTGGTGA GTCTGGGGT GGCCTGGTC AGCAGGGG CTCACCTCCGT
ACGTAGATAC AAGCAAAAA GATAACGATG TTTGGCGATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCAG TCGTCCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R

*Anti-Tissue Factor Heavy Chain

1701 TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGGAGTACT ACATGCACTG GTCCGCTCAG GCGCCGGGTA AGGGCCTGGA ATGGTTTGA TTGATTGATC
AACAGGACAC GTCGAAGACC GAAGTTATTA TTTCTCATGA TGTACGTGAC CCAGGCAGTC CCGGCCCCAT TCCCGACCT TACCCAACT AACTAACTAG
43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P

1801 CAGAGCAAGG CAACAGCATC TATGACCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA TACCTGCAGA TGAACAGCCT
GTCTCGTTCC GTTGTGCTAG ATACTGGCT TCAAGGTCCT GGCACGGTGA TATTCGGAC TGTAAAGTT TTTGTCTGT ATGGACGTCT ACTTGTGGA
77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L

1901 GCGTGTCTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCTGG TCACCGTCTC CTCGGCCTCC
CGCAGGACTC CTGTGACGGC AGATNATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCAGTT CTTGGGACC AGTGGCAGAG GAGCCGGAGG
110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S

2001 ACCAAGGGCC CATCGGTCTT CCGCTTGGCA CCCTCTTCCA AGAGCACCTC TGGGGGACA GCGGCCCTGG GCTGCTGTGT CAAGGACTAC TTCCCCGAAC
TGGTTCCCGG GTAGCCAGAA GGGGACCGT GGGAGGAGT TCTCGTGGAG ACCCCGCTGT CCGCGGGACC CGACGGACCA GTTCTGTATG AAGGGGCTTG
143 T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P

2101 CCGTGACGGT GTCGTGGAAC TCAGGGGCCC TGACCAGCGG CGTGACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCTCTGAG ATGAGGAGT CGTCGCACCA
177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V

2201 GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA AGAAAGTTGA GCCCAAATCT
CTGACACGGG AGATCGTCCA ACCCGTGGT CTGGATGTAG ACGTTGCACCT TAGTGTTCGG GTCGTTGTGG TTCCACCTGT TCTTCACT CGGGTTTAGA
210 T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S

2301 TGTGACAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCTTGG GGGACCGTCA GTCTTCTCT TCCCCCAA ACCCAAGGAC ACCCTCATGA
ACACTGTTTT GAGTGTGTAC GGGTGGCAG GGTGTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGACA AGGGGGTTT TGGTTCCTG TGGGAGTACT
243 C D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I

FIG. 1C

2401 TCTCCCGGAC CCTGAGGTC ACATCGGTGG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGTACGTG GACGGCGTGG AGGTGCATAA
AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGCTT CTGGGACTCC AGTTCAAGTT GACCATGCAC CTGCCGCACC TCCACGTATT
277 S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N

2501 TGCCAAGACA AAGCCGCGG AGGAGCAGTA CAACAGCAGC TACCSTGTGG TCAGCGTCTT CACCGTCTCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC
ACGGTCTGT TTCGGCGCCC TCCTCGTCTAT GTTGTCTGTC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCTCTGA CCGACTTACC GTTCTCTCATG
310 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y

2601 AAGTGCAGG TCTCCAACA AGCCCTCCCA GCCCCCATCG AGAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC
TTCACGTTC AGAGTTGTT TCGGGAGGGT CCGGGGTAGC TCTTTGGTA GAGGTTTCGG TTTCCCGTCTG GGGCTCTTGG TGTCCACATG TGGGACGGGG
343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P

2701 CATCCCGGGA AGAGATGACC AAGAACAGG TCAGCTGAC CTGCTGTGTC AAAGGCTTCT ATCCCAGCGA CATGCCCGTG GAGTGGGAGA GCAATGGGCA
GTAGGCCCC TCTCTACTGG TTCTTGGTCC AGTCGACTG GACGGACCAG TTTCGGAAGA TAGGCTCGT GTAGGGGCAC CTCACCTCT CTTACCCGT
377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q

2801 GCCGAGAAC AACTACAAGA CCACGCTCC CGTGTGGAC TCCGACGGCT CCTTCTTCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
CGSCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGCTGCCGA GGAAGAAAGA GATGCTGTT CAGTGGCACC TGTCTCTGTC CACCGTCGTC
410 P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q O

2901 GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGAGAGG AGCCTCTCCC TGTCTCCGG TAAATAAGCA TCGCAGCGCC
CCCTTGACAG AGAGTACGAG GCACTACGTA CTCGAGAGCG TGTGTGTAT GTGCTCTTC TCGGAGAGGG ACAGAGGCCC ATTTATTCGT ACCCTGCCGG
443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O

3001 CTAGAGTCCC TAACGCTCGG TTGCCGCGG CGGTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTT AATGCGGTAG TTTATCACAG
GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAT AACAAATTGAG TACAAACTGT CGAATAGTAG CTATTGAAA TTACGCCATC AAATAGTGT
3101 TTAATTGCT AACGCAGTCA GGCACCGTGT ATGAATCTA ACAATGCGCT CATGCTCATC CTCGGCACCG TCACCTCTGA TGTGTAGGC ATAGGCTTGG
AATTAAACGA TTGCGTCACT CCGTGGCACA TACTTTAGAT TGTACGCGA GTAGCAGTAG GAGCCGTGGC AGTGGGACCT AGGACATCCG TATCCGAACC

*Start Tet Resistance Coding Sequence

3201 TTATGCCGT ACTGCCGGC CTCTTGCGG ATATCGTCCA TTCCGACAGC ATCCCCAGTC ACTATGGCGT GCTGTAGCG CTATATGCGT TGATGCAATT
AATACGGCCA TGACGGGCCG GAGAACGCC TATAGCAGGT AAGGCTGTG TAGCGGTGAG TGATACCGCA CGACGATCGC GATATACGCA ACTACGTTAA

FIG. 1D

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTATG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GGCAGAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC CGGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCACTA
CCCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GACGAGTCAT

301 AAAAGTTAAT CTTTTCACAA GCTGTCAFAA AGTTGTCAAG GCCGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTTGTAACCTA GTACGCAAGT
TTTTCATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGTATCTA GAATTATGAA GAAAAACATC GCTTTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
AGTGCATTTT TCCCATAGAT CTTAATACTT CTTTTTGTAG CGAAAAGAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGGGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^start STII signal TIR-2 start light chain^

501 CAGATGACCC AGTCCCGGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACG TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAACTGGT
GTTCTACTGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTG AGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAGAC TTGCGAACTT ATTACTGTCT TCAGCACGGA GAGTCTCCAT GGACATTTGG ACAGGGTACC
CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCTT CTCAGAGGTA CCTGTAAACC TGTCCCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

801 AAGGTGGAGA TCAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTGTGT GTGTGCCTGC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

FIG. 2A

901 TGAATAACTT CTATCCCAGA GAGGCCAAG TACAGTGGA GGTGGATAAC GCCCTCCAAT CGGTAATC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGAGAGTTA GCCCATTTGAG GGTCTCTCTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACAGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTCGAGT CGTCGCTGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGAGC CATCGTGGG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
AGCGGGCAGT GTTCTCTGAA GTTGTCTGAA GTTGTCTGCT CTCACAAATTA ATTTAGGAGA TCGGCGCTGC GTAGCACCGC TCGAGCCATG GGCCCTCTAGA TCCGGATTGC
226 S P V T K S F N R G E C O

1201 CTCGGTTGCC GCGGGCGTT TTTTATTGTT GCGGACGGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
GAGCCCAACGG CGGCCCGCAA AAAATAACAA CCGCTGCGG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCAATATGG CGCAAAATGA CCAACACGG TTGATTGATC AGGTAGAGG GCGCTGTAC GAGTAAAG CCGATGCCAG CATTCCTGAC GAGCATACGG
CGGTTATACC GCCTTTTACT GGTTGTCGCC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTTC GGCTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACAG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATT CAACAGTGCC GGCTCTGAAT

1501 TAGTCGCTTT GTTTTATT TTGTAATGAT TACGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAAACATCG CTTTCTCTCT
ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTT CCCATAGATC TTAATACTTC TTTTGTAGC GAAAAGAAGA
1 M K K N I A F L L
^start STII signal TIR-2

1601 TGCATCTATG TTCGTTTTT CTATTGCTAC AAACGGGTAC GCTGAGGTT ACCTGGTGA GTCTGGCGGT GGCCTGTGTC AGCCAGGGGG CTCACCTCCGT
ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGGCGATG CGACTCCAAG TCGACCACTT CAGACCGCCA CCGGACCAAG TCGGTCCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R
^start heavy chain

FIG. 2B

1701 TTGTCCTGTG CAGCTTCTCG CTTCATATTT AAGGAGTACT ACATGCAC TGTCGGCTCAG GCGCCGGGTA AGGCGCTGGA ATGGGTGGA TTGATGTATC
AACAGGACAC GTCGAAGACC GAAGTTATAA TTCTCTATGA TGTACGTGAC CCAGGCAGTC CCGGGCCCAT TCCCGACCT TACCCAACCT AACFAACTAG
43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P

1801 CAGAGCAAGG CAACACGATC TATGACCCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA TACCTGCAGA TGAACAGCCT
GTCTGTTCC GTTGCTGTAG ATACTGGCT TCAAGGTCCT GGCACGGTGA TATTCCGAC TGTAAAGTT TTTGTGCTGT ATGGACGTCT ACTTGTGCGA
77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L

1901 GCGTGTGAG GACACTGCGG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCCCTGG TCACCGTCTC CTCGGCCTCC
CGCAGGACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCAGTT CTTGGGACC AGTGGCAGAG GAGCCGGAGG
110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S

2001 ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGTT CAAGGACTAC TTCCCCGAAC
TGTTCCCGG GTAGCAGAA GGGGACCGT GGGAGGAGT TCTCGTGAG ACCCCCGTGT CCGCGGACC CGACGGACCA GTTCTGTATG AAGGGCTTG
143 T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P

2101 CGGTGACGGT GTCGTGGAAC TCAGGGCGCC TGACCAGGG CGTGACACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGTCGCC GCACGTGTGG AAGGGCGAC AGGATGTGAG GAGTCTGAG ATGAGGGAGT CGTCGCACCA
177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V

2201 GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAGCC CAGCAACACC AAGGTGACA AGAAAGTTGA GCCCAAATCT
CTGACACGGG AGATCGTGA ACCCGTGGT CTGGATGTAG ACGTTGCACT TAGTGTGCG GTCTGTTGG TTCCACCTGT TCITTCAACT CGGGTTTGA
210 T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S

2301 TGTGACAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCTCT TCCCCCANA ACCCAAGGAC ACCCTCATGA
ACACTGTTTT GAGTGTGTAC GGTGTGCACG GGTGTGCAC TTGAGACCC CCCTGGCAGT CAGAAAGAGA AGGGGGTTT TGGGTCTCTG TGGGAGTACT
243 C D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I

2401 TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCAGAA GACCCTGAGG TCAAGTTCAA CTGTTAGTGG GACGGCGTGG AGGTGCATAA
AGAGGGCCTG GGGACTCCAG GTTAGGCACC ACCACTGCA CTCGGTGTCT CTGGACTCC AGTTCAAGTT GACCATGCAC CTGCGGACCC TCCACGTATT
277 S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N

FIG. 2C

2501 TGCCAAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCAGC TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC
ACGGTTCTGT TTCGGCGCCC TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA GTGGCTCTGA CCGACTTACC GTTCCTCATG
310 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y
2601 AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GCGCCCATCG AGAAAACCAT CTCCAAGGCC AAAGGCAGC CCCAGAAACC ACAGTGTAC ACCCTGCCCC
TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CCGGGGTAGC TCTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTGG TGTCACATG TGGGACGGGG
343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P
2701 CATCCCCGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA
GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGGACTG GACGGACCAG TTTCGGAAGA TAGGTCGCT GTAGCGGCAC CTCACCTCT CATTACCGT
377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q
2801 GCCGGAGAAC AACTACAAGA CCACGCCCTCC CGTGCTGGAC TCCGACGGCT CTTCTTCTCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
CGGCTCTCTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTT CAGTGGCACC TGTCTCGTC CACCGTCGTC
410 P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q
2901 GGGAACGTCT TCTCATGCTC CGTGATGCTC GAGGCTCTGC ACAACCACTA CAGCAGAAG AGCCTCTCCC TGTCTCCGG TAAATAAGCA TGGGACGGCC
CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTGCTGAT GTGCGTCTTC TCGGAGAGGG ACAGAGGCC CATTATTCTG ACGTGTCCGG
443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O
3001 CTAGAGTCCC TAACGCTCGG TTGCCGCGCG GCGTTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT AATCGGTAG TTTATCACAG
GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAATTGAG TACAAACTGT CGAATAGTAG CTATTGAAA TTACGCCATC AATATGTC
3101 TTAATTTGCT AACGCAGTCA GGCACCGTGT ATGAAATCTA ACAATGCGCT CATCGTCATC CTCGGCACCG TCACCCCTGA TCGTGTAGGC ATAGGCTTGG
AATTTAAGCA TTGCGTCACT CCGTGGCACA TACTTTAGAT TGTTACGCGA GTAGCAGTAG GAGCCGTGGC AGTGGGACCT ACGACATCCG TATCCGAACC
3201 TTATGCCGGT ACTGCCGGGC CTCTTGCGGG ATATCGTCCA TT
AATACGGCCA TGACGGCCCG GAGAACGCC TATAGCAGGT AA

FIG. 2D

1 GAATTCAACT TCTCCATACT TTGGATAAGG AATATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCGATGCCA GCATTCTCTGA CGACGATAGG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT CTTGCTATGC CTCGACGAGG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCTATA AGTTGTCAAG GCCGAGACTT ATAGTCGCTT TGTTTTTTATT TTTTAATGTA TTTGTAAC TA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAA AGGTATCTA GAATTATGAA GAAGAATATC GCATTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
AGTGCAATTT TCCCATAGAT CTTAATACCT CTTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
STII Signal TIR -1 Anti-VEGF Light chain

501 CAGTTGACCC AGTCCCCGAG CTCCTGTGTC GCGTAGGGT CACCATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAAACTGGT
GTCAACTGGG TCAGGGGCTC GAGGACAGC CGGTATCCCA GTGCTAGTGG ACCTGCGGTT CAGTCCTATA ATCGTTGATA AATTTGACCA

26 Q L T Q S P S S L S A S V G D R V T I T C S A S Q D I S N Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTTCACTCC TCTCTCCACT CTGAGTCCC TTCTCGCTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTT ATGACTAAAT GAAGTGGAGG AGAGAGGTGA GACCTCAGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y F T S S L H S G V P S R F S G S G S G T

701 GGATTTCACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCA ACAGTATAGC ACCGTGCCGT GGACGTTTG ACAGGTATCC
CCTAAAGTGA GACTGGTAGT CGTCAGACGT CCGTCTTCTG AAGCGTTGAA TAATGACAGT TGTCTATATCG TGGCAGCGCA CCTGCAAAACC TGTCCTCATGG

93 D F T L T I S S L Q P E D F A T Y Y C Q Q Y S T V P W T F G Q G T

801 AAGGTGGAGA TCAACGAAC TGTGGTGC CACTCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC
TTCCACCTCT AGTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

FIG. 3A

901 TGAATAACTT CTATCCAGA GAGGCCAAG TACACTGGA GGTGGATAAC GCCCTCCAAT CCGGTAAC TC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGGTCT CTCGGGTTTC ATGTCACCTT CCACCTATTG CCGGAGGTTA GCCCATTCAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K
1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGGGAG TCACCCATCA GGGCCTGAGC
CCTGCTGTGG ATGTGGGAGT CGTCGTGGGA CTGGCACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CCGACGCTTC AGTGGGTAGT CCGGCACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S
1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAT TAAATCCTCT ACGCCGGAGC CATCGTGGG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
AGCGGGCAGT GTTCTCGAA GTTGTCCTCT CTCACAAATTA ATTTAGGAGA TGCGGCTGCG GTAGCACCGC TCGAGCCATG GGGCCCTAGA TCCGGATTCG
226 S P V T K S F N R G E C O
1201 CTCGGTTGCC GCGGGCGTT TTTTATTGTT GCCGACGCG ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
GAGCCACCG CCGCCCGCAA AAAATAACAA CCGCTGCGG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA
1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGG GCGCTGTAC GAGGTAAGC CGATGCCAG CATTCCTGAC GACGATACGG
CGGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTCC GGTACGGTC GTAAGGACTG CTGCTATGCC
1401 AGCTGCTGCG CGATTACGTA AAGAAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACCG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATT CAACAGTGCC GGTCTGAAT
1501 TAGTCGCTTT GTTTTATTT TTTAATGTAT TTGTAAGTAG TAGGCAAGTT CACGTAATAA GGTATCTAG AATTATGAAG AAGAATATCG CATTTCTTCT
ATCAGGAAA CAAAAATAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTT CCCATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
1 M K K N I A F L L
^STII Signal TIR-1
1601 TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGGGTAC GCTGAGGTC AGCTGGTGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACTCCGT
ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCCAG TCGGTCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R
^Anti-VEGF Heavy Chain

FIG. 3B

1701 TTGTCCTGTG CAGCTTCTGG CTACGACTTC AGCAGCTAGG GTATGAACTG GGTCGGTCAG GCCCGGGTA AGGCGCTGGA ATGGGTTGGA TGGATTAACA
AACAGGACAC GTCGAAGACC GATGCTGAAG TCGGTGATGC CATACTTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT TACCCAACCT ACCTAATTGT
43 L S C A A S G Y D F T H Y G M N W V R Q A P G K G L E W V G W I N T
1801 CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG TCGTTTCACT TTTTCTTTAG ACACCTCCAA AAGCACAGCA TACCTGCAGA TGAACAGCCT
GGATATGGCC ACTTGGCTGG ATACGACGCC TAAAGTTTGC AGCAAGTGA AAAGAAATC TGTGGAGTTT TTCTGTCTGT ATGGACGTCT ACTTGTTCGGA
77 Y T G E P T Y A A D F K R R F T F S L D T S K S T A Y L Q M N S L
1901 GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC CCGTACTATT ACGGCACGAG CCACTGGTAT TTCGACGTCT GGGTCAAGG AACCTTGGTC
CGCGGACTC CTGTGACGGC AGATAATGAC AGTTTTCATG GGCATGATAA TGCCGTGCTC GGTGACCATA AAGCTGCAGA CCCCAGTTCC TTGGGACCAG
110 R A E D T A V Y Y C A K Y P Y Y Y G T S H W Y F D V W G Q G T L V
2001 ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCTGTGCCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGC TGCCCTGGTCA
TGGCAGAGGA GCCGGAGGTG GTTCCCGGGT AGCCAGNAGG GGGACCGTGG GAGGAGGTTT TCGTGGAGAC CCCCCTGTGCG CCGGGACCCG ACGGACCAGT
143 T V S S A S T K G P S V F P L A P S S K S T S G T A A L G C L V K
2101 AGGACTACTT CCCCAGAACG GTGACGGTGT CGTGGAATC AGGGCCCTG ACCAGCGGG TGCACACCTT CCCGGCTGTC CTACAGTCTT CAGGACTCTA
TCCTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG TCCCGGGGAC TGGTCGCCGC ACGTGTGGAA GGGCCGACAG GATGTCAGGA GTCTTGAGAT
177 D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y
2201 CTCCTCAGC AGCGTGGTGA CTGTGCCCTC TAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG
GAGGAGTCG TCGCACCACT GACACGGGAG ATCGTCGAAC CCGTGGTCT GGTGACTTA GTTGACTAGAC GTTTCGGGT CGTTGTGGTT CCACCTGTTT
210 S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K
2301 AAAGTTGAGC CCAATCTTG TGACAAAACCT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGG GACCGTCAGT CTTCTCTTTC CCCCCAAAAC
TTTCAACTCG GGTTAGAAC ACTGTTTGA GTGTGTACGG GTGGCAGGG TCGTGGACTT GAGGACCCCT CCGCAGTCA GAAGGAGAAG GGGGTTTTG
243 K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P P K P
2401 CCAAGGACAC CCTCATGATC TCCCGGACCC CTGAGGTGAC ATGGTGGTG GTGGACGTGA GCCACGAAGA CCTGAGGTG AAGTTCAACT GGTACGTGGA
GGTTCCTGTG GGAGTACTAG AGGGCCTGGG GACTCCAGTG TAGGCACCAC CACCTGCACT CCGTGTCTT GGGACTCCAG TTCAAGTTGA CCATGCACCT
277 K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V D

FIG. 3C

2501 CGGCGTGGAG GTGCATAATG CCAAGACAAA GCCGGGGGAG GAGCAGTACA ACAGCAGCTA CCGTGTGGTC AGCGTCTCTA CCGTCTCTGCA CCAGGACTGG
GCCGCACCTC CAGGTATTAC GGTTCTGTTT CGGCGCCCTC CTCGTCAATG TGTCTGTCAT GGCACACCAG TCGCAGGAGT GGCAGGACGT GGTCTGTACC
310 G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W

2601 CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAG CCTCCCCAGC CCCCATCGAG AAACCATCT CCAAGGCCAA AGGCAGCCCC CGAGAACCAC
GACTTACCGT TCCTCATGTT CAGGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGTAGCTC TTTTGGTAGA GGTTCGGTT TCCCGTCGGG GCTCTTGGTG
343 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q

2701 AGGTGTACAC CCTGCCCCCA TCCCGGGAAG AGATGACCAA GAACCAGGTC AGCTGACCT GCCTGGTCAA AGGCTTCTAT CCAGCGCACA TCGCCGTGGA
TCCACATGTG GGACGGGGGT AGGCCCTTC TCTACTGTT TCTGGTCCAG TCGGACTGGA CGGACCAGTT TCCGAAGATA GGTCTGCTGT AGCGGCACCT
377 V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E

2801 GTGGAGAGC AATGGGCAGC CGGAGAACA CTACAGACC AGCCTCCCG TGTGGACTC CGACGGCTCC TTCTTCTCT ACAGCAAGCT CACCGTGGAC
CACCTCTCG TTACCCGTCG GCCTCTGTT GATGTTCTGG TCGGAGGGC AGACCTGAG GCTGCCGAGG AAGAAGGAGA TGTCTTCTGA GTGGCACCTG
410 W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D

2901 AAGAGCAGGT GGCAGCAGG GAAGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCCTTACA CGCAGAAGAG CTCTCCCTG TCTCCGGGTA
TTCTCGTCCA CCGTCGTCC CTTGCAGAAG AGTACGAGC ACTACGTACT CCGAGACGTG TTGGTATGT GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT
443 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K

3001 AATAAGCATG CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGG GTTTTTTATT GTTAACTCAT GTTGCACAGC TTATCATCGA TAAGCTTTAA
TTATTCTGAC GCTGCCGGGA TCTCAGGGAT TCGAGGCCAA CGCGGGCCCG CAAAAATAA CAATTGAGTA CAACTGTCTG AATAGTAGCT ATTCGAAATT
477 O

3101 TCGGAGTATT TATCAGAGTT AAATTGCTAA CGCAGTCAGG CACCGTGAT GAAATCTAAC AATGGCTCA TCGTCACTCT CGGCACCGTC ACCCTGGATG
ACGCCATCAA ATAGTGTCAA TTTAAGGATT GCGTCAGTCC GTGGCACATA CTTTAGATTG TTACGGAGT AGCAGTAGGA GCCGTGGCAG TGGGACCTAC
^Start Tet Resistance Coding Sequence

3201 CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCCT CTTGGGGAT ATCGTCCATT CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT
GACATCCGTA TCCGAACCAA TAGGGCCATG ACGGCCCGGA GAACGCCCTA TAGCAGGTAA GGCTGCTGTA GCGTCTAGTG ATACCGCAGC ACGATCGCGA

FIG. 3D

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1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAGAAGA AGAGTCGAAT
  CTTAAGTTGA AGAGGTATGA AACCTATTCC TTATATGCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACTGTGTG GCGAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
  CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTGTGCGC CAACTAACATA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
  CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA GCTGTCATAA AGTTGTCACG GCGAGACCTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTGTAACTA GTACGGCAAGT
  TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATCGCTTCA

401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTCTCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
  AGTGCATTTT TCCCATAGAT CTTAATACCTT CTTCTTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTGGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I ^Light chain
  ^STII signal TIR -1

501 CAGTTGACCC AGTCCCGCAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAAGTGGT
  GTCAACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG AGTCTCGGTT CAGTCTCTATA ATCGTTGATA AATTGACCA

26 Q L T Q S P S S L S A S V G D R V T I T C S A S Q D I S N Y L N W Y

601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTTACCTCC CTCTCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
  TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GAAGTGGAGG AGAGAGGTGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y F T S S L H S G V P S R F S G S G T

701 GGAATTCAC CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTGCGAACTT ATTACTGTCA ACAGTATAGC ACCGTGCCGT GGACGTTTGG ACAGGGTACC
  CCTAAAGTGA GACTGGTAGT CGTCAGACGT CCGTCTTCTG AAGCGTTGAA TAATGACAGT TGTATATCG TGGCAGGCA CCTGCAAAACC TGTCCTCATGG

93 D F T L T I S S L Q P E D F A T Y Y C Q Q Y S T V P W T F G Q G T

801 AAGGTGGAGA TCAAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
  TTCCACCTCT AGTTTGCTTG ACACCGAGGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

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FIG. 4A

901 TGAATAACTT CTATCCAGA GAGGCCAAG TACAGTGGAA GGTGATAAC GCCCTCCAAT CCGGTAATC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACTTT CCACCTATTG CCGGAGGTTA GCCCATTTAG GGTCTCTTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCCAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTGT GTTTCAGATG CCGACGCTTC AGTGGTAGT CCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGAGC CATCGTGGC AGCTCGGTAC CCGGGATCT AGGCCATAACG
AGCGGGCAGT GTTCTCTGAA GTTGTCCTCT CTCACAATTA ATTAGGAGA TCGCGCCTGC GTAGCACCGC TCGAGCCATG GGCCCTTAGA TCCGGATTGC
226 S P V T K S F N R G E C O

lambda to terminator

1201 CTCGGTTGCC GCCGGGGCTT TTTTATTGT GCCGACGGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
GAGCCACGG CGGCCCGCAA AAAATAACAA CGGCTGGCG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCAATATGG CGCAAAATGA CCAACAGCG TTGATTGATC AGGTAGAGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCTGAC GACGATACGG
GCGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCCATCTCCC CCGGACATG CTCATTTTCG GGTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACGG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGCTCTGAAT

1501 TAGTCGCTTT GTTTTATTT TTAAATGAT TTGTAAGTAC TAGGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAGAATATCG CATTCTTCT
ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTT CCGATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
1 M K K N I A F L L
^STII Signal TIR-1

1601 TGCATCTATG TTCGTTTTT CTATTGCTAC AAACGGGTAC GCTGAGGTT CAGTGGTGA GTCTGGGGT GGCCTGGTGC AGCAGGGGG CTCACTCGGT
ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGGCGATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG TCGGTCCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R
^start heavy chain

FIG. 4B

1701 TTGTCCTGTG CAGCTTCTGG CTATACCTTC ACCAACTATG GTATAAAGTGGTCCGTCAG GCGCCGGGTA AGGCCCTGGA ATGGGTTGGA TGGATTAAACA
AACAGGACAC GTCGAAGACC GATATGAAG TGGTTGATAC CATATTGAC CCAGGCAGTC CCGGGCCCAT TCCCGGACCT TACCCAACCT ACCTAATTGT
43 L S C A A S G Y T F T N Y G I N W V R Q A P G K G L E W V G W I N T
1801 CCTATACCGG TGAACCGACC TATGCTGGG ATTTCAAAG TCGTTTCACT TTTTCTTAG ACACCTCCA AAGCACAGCA TACCTGCAGA TGAACAGCCT
GGATATGGCC ACTTGCTGG ATACGACGCC TAAAGTTGC AGCAAAGTGA AAAAGAAATC TGTGGAGGT TCGTGTCGT ATGGACGTCT ACTTGTCGGA
77 Y T G E P T Y A A D F K R R F T F S L D T S K S T A Y L Q M N S L
1901 GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC CCGCACTATT ATGTGAACGA GCGGAAGAGC CACTGGTATT TCGACGTCTG GGGTCAAGGA
CGCGCGACTC CTGTGACGGC AGATAATGAC ACGTTTCATG GCGGTGATAA TACACTTGCT CGCCTTCTCG GTGACCATAA AGCTGCAGAC CCCAGTTCTT
110 R A E D T A V Y Y C A K Y P H Y Y V N E R K S H W Y F D V W G Q G
2001 ACCCTGGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CCGTCTTCCC CCGTGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT
TGGGACCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAAGGG GGACCGTGGG AGGAGTTCT CGTGGAGACC CCGGTGTCCG CCGGACCCGA
143 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C
2101 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGC GTGGAATCA GCGCCCTGTA CCAGCGGGGT GCACACCTTC CCGGTGTCC TACAGTCTTC
CGGACCAGTT CCGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTGCGCGCA CGTGTGGAAG GCGCGACAGG ATGTCAGGAG
177 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S
2201 AGGACTCTAC TCCTCAGCA GCGTGGTGAC TGTGCCCTCT AGCAGTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCAG CAACACCAAG
TCCTGAGATG AGGAGTCTGT CGACCACTG ACACGGGAGA TCGTGAAC TCGTGGTCTG GATGTAGAGG TTGCACCTAG TGTTCGGGTC GTTGTGGTTC
210 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K
2301 GTGGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGG ACCGTGATC TTCCTCTTCC
CACCTGTTCT TTCAACTCGG GTTTAGAACA CTGTTTGGAG TGTGTACGGG TGGACGGGT CGTGGACTTG AGGACCCCCC TGGCAGTCAG AAGGAGAAGG
243 V D K K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P
2401 CCCCCAAACC CAAGGACACC CTCATGATCT CCGGACCCC TGAGGTCA TCGGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG
GGGGTTTTGG GTTCCTGTGG GAGTACTAGA GGGCCCTGGG ACTCCAGTGT ACGCACACC ACCTGCATC GGTGCTCTG GGACTCCAGT TCAAGTTGAC
277 P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W

FIG. 4C

2501 GTACGTGGAC GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC CGTGTGGTCA GCGTCTCAC CGTCTGAC
CATGCACCTG CCGCACCTCC AGTATTACG GTTCTGTTTC GCGCCCTCC TCGTCATGTT GTCGTGCATG GCACACCAGT CCGAGGAGTG GCAGGACGTG
310 Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H

2601 CAGGACTGGC TGAATGGCAA GGAGTACAAAG TGCAAGGTCT CCAACAAAGC CCTCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA GGGCAGCCCC
GTCCTGACCG ACTTACCGTT CCTCATGTTT ACCTTCCAGA GGTGTTTCG GGAGGTCCG GGGTAGCTCT TTTGGTAGAG GTTTCGGTTT CCGTCGGGG
343 Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R

2701 GAGAACACCA GGTGTACACC CTGCCCCCAT CCGGGGAAGA GATGACCAAG AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT
CTCTGGTGT CCACATGTGG GACGGGGTA GGGCCCTTCT CTACTGTTTCT TTGGTCCAGT CGGACTGGAC GGACCAGTTT CCGAAGATAG GGTGCTGTA
377 E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I

2801 CCGCGTGGAG TGGGAGACA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC GACGGTCTCT TCTTCTCTA CAGCAAGCTC
GGGCACCTC ACCCTCTCGT TACCCGTCGG CCTCTTGTG ATGTTCTGGT GCGGAGGCA CGACCTGAGG CTGCCGAGGA AGAAGGAGAT GTCGTTCCG
410 A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L

2901 ACCGTGGACA AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT
TGGCACCTGT TCTCGTCCAC CGTCGTCCCC TTGCAGAAGA GTACGAGGCA CTACGTACTC CGAGACGTGT TGGTGATGTG CGTCTTCTCG GAGAGGGACA
443 T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S

3001 CTCGGGGTAA ATAAGCATGC GACGGGCCCTA GAGTCCCTAA CGCTCGGTTG CCGCCGGGGG TTTTATTG TTAACATG TTTGACAGCT TATCATCGAT
GAGGCCATT TATTCTACG CTGCCGGGAT CTCAGGGATT GCGAGCCCAAC GCGGCCCGC AAAAAATAAC AATTGAGTAC AAAGTGCGA ATAGTAGCTA
477 P G K O ^lambda terminator

3101 AAGCTTTAAT GCGGTAGTTT ATCACAGTTA AATTGCTAAC GCAGTCAGC ACCGTGTATG AAATCTAACA ATGGCTCAT ATGCATCTC GGCACCGTCA
TTGGAATTA CGCCATCAA TAGTGTCAT TTAACGATTG CGTCAGTCCG TGGCACATAC TTTAGATTGT TACGCGAGTA GCAGTAGGAG CCGTGGCAGT

3201 CCTGGATGC TGTAGCATA GGCTTGGTTA TGCCGGTACT GCCGGGCCCTC TTGCG
GGGACCTACG ACATCGGTAT CCGAACCAAT ACGGCCATGA CCGCCCGGAG AACGC

FIG. 4D

1 ATCGATGAAT TCATGCTGTG GTGTCAATGGT CCGTGATCGC CAGGGTGCCG ACGGCGATCT CGACTGCAGG GTGCACCAAT GCTTCTGGCG TCAGGCAGCC
TAGCTACTTA AGTACGACAC CACAGTACCA GCCACTAGCG GTCCACCGC TCGCGGTAGA GCTGACGTGC CACGTGGTTA CGAAGACCGC AGTCCGTGGG
^ClaI

101 ATCGAAGCT GTGGTATGGC TGTGCAGGTC GTAAATCACT GCATAATTCG TGTGCTCAA GGGGCATCC CGTCTCGAT AATGTTTTT GCGCCGACAT
TAGCCTTGA CACCATACCG ACACGTCCAG CATTTAGTA CGTATTAGC ACAGCGAGTT CCGCGTGAGG GCAAGACCTA TTACAAAAA CGCGGCTGTA

201 CATAACGGTT CTGGCAATA TTCTGAAATG AGCTGTTGAC AATTAATCAT CGAATAGTT TAATGTGGG AATTGTGAGC GGATAACAAT TAAGCTTAGG
GTATTGCCAA GACCGTTTAT AAGACTTTAC TCGACAACTG TTAATTAGTA GCTTGATCAA ATTACACACC TTAACACTCG CCTATTGTTA ATTCGAATCC

301 ATTCTAGAGG GAAGATTTAT GAAATCACTG TTAAAGTAA CGCTGCTGGC GACCACAATG GCCGTTGCC TGCATGCACC AATCACTTTT GCTGCTGAAG
TAAGATCTCC CTTCTAAATA CTTTAGTGAC AATTTTCAAT GCGACGACCG CTGGTGTTAC CGGCAACGGG ACGTACGTGG TTAGTGAATA CGACGACTTC
1 M K S L F K V T L L A T T M A V A L H A P I T F A A E A
^fkpA start

401 CTCGAAAACC TGCTACAGCT GCTGACAGCA AAGCAGCGTT CAAAATGAC GATCAGAAAT CAGCTTATGC ACTGGTGCC TCGCTGGGTC GTTACATGGA
GACGTTTGG ACGATGTCGA CGACTGTCGT TTGCTGCGAA GTTTTACTG CTAGTCTTA GTCGAATACG TGACCCACGG AGCGACCCAG CAATGTACCT
29 A K P A T A A D S K A A F K N D D Q K S A Y A L G A S L G R Y M E

501 AAACCTCTTA AAAGAACAAG AAAAAGTGG CATCAAACTG GATAAAGATC AGCTGATGC TGGTGTTCAG GATGATTTG CTGATAAGAG CAAACTCTCC
TTTGAGAGAT TTCTTTGTTT TTTTGGACCC GTAGTTTGAC CTATTCTAG TCGACTAGCG ACCACAAGTC CTACGTAAAC GACTATTCTC GTTTGAGAGG
62 N S L K E Q E K L G I K L D K D Q L I A G V Q D A F A D K S K L S

601 GACCAAGAGA TCGAACAGAC TCTACAAGCA TTGCAAGCTC GCGTGAAGTC TTCTGCTCAG GCGAAGATGG AAAAAGACGC GGCTGATAAC GAAGCAAAAG
CTGGTTCTCT AGCTTGCTG AGATGTTTCTG AAGCTTCGAG CGCACTTCAG AAGACGAGTC CGCTTCTACC TTTTCTGCG CCGACTATTG CTTCTGTTTC
95 D Q E I E Q T L Q A F E A R V K S S A Q A K M E K D A A D N E A K G

701 GTAAAGAGTA CCGCGAGAAA TTTCGCAAG AGAAGGTGT GAAACCTCT TCAACTGGTC TGGTTTATCA GGTAGTAGAA GCCGGTAAAG GCGAAGCACC
CATTTCTCAT GCGCTCTTTT AAACGGTTTC TCITTCCACA CTTTGGAGA AGTTGACCAG ACCAAATAGT CCATCATCTT CGGCATTTT CCGCTTCTGG
129 K E Y R E K F A K E K G V K T S S T G L V Y Q V V E A G K G E A P

FIG. 5A

801 GAAAGACAGC GATACTGTTG TAGTGAAC TA CAAAGGTACG CTGATCGACG GTAAAGAGTT CGACAAC TCT TACACCCG TG GTGAACCGCT TTCTTTCCGT
CTTTCTGTG CTATGACAC ATCACTTGAT GTTTCATGC GACTAGCTGC CATTTCTCAA GCTGTTGAGA ATGTGGGCAC CACTTGGCGA AAGAAAGGCA
162 K D S D T V V V N Y K G T L I D G K E F D N S Y T R G E P L S F R
901 CTGGACGGTG TTATCCCGGG TTGGACAGAA GGTCTGAAGA ACATCAAGAA AGCGGTAAG ATCAAACTGG TTATTCCACC AGAAGTGGCT TACGGCAAAG
GACCTGCCAC AATAGGGCCC AACCTGTCTT CCAGACTTCT TGTAGTTCTT TCCGCCATTG TAGTTTGACC AATAAGGTGG TCTTGACCGA ATGCCGTTTC
195 L D G V I P G W T E G L K N I K K I K L V I P P E L A Y G K A
1001 CGGGTGTTC GGGATCCCA CCGAATTCTA CCCTGGTGTG TGACGTAGAG CTGCTGGATG TGAACCAGC GCCGAAGGCT GATGCAAAGC CGGAAGCTGA
GCCCCAAGG CCCCTAGGGT GGCTTAAGAT GGGACCACAA ACTGCATCTC GACGACCTAC ACTTTGGTGG CGGCTTCCGA CTACGTTTCG GCCTTCGACT
229 G V P G I P P N S T L V F D V E L L D V K P A P K A D A K P E A D
1101 TCGGAAGCC GCAGATTCTG CTAAAAATA AAGCTAGC
ACGCTTTCGG CGTCTAAGAC GATTTTAT TTTGATCG
262 A K A A D S A K K O
*NheI

FIG. 5B

1 GAATTCAACT TCTCCAFAC TGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCIG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA
^EcoRI

101 GAACCTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTGCG CAACCTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCCTGA CGACGATPAC GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACCTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCAATA AGTTGTCAGG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGTATCTA GAATTATGAA AAAGAATATC GCATTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGTA CGCTGATATC
AGTGCATTT TCCCATAGAT CTTAATACTT TTTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTGGCGCAT CGGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^start STII signal TIR 7 anti-TF light chain^

501 CAGATGACCC AGTCCCGGAG CTCCTGTGTC GCGATAGGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAACCTGGT
GTCTACTGGG TCAGGGGCTC GAGGACAGG CGGACACACC CGCTATCCCA GTGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGCTG AAGGATCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GATAGGATGA TCAGAGCGAC TTCTCAGGG AAGAGCGAAG AGACTAGGC CAAGACCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTGCAACTT ATTACTGTCT TCAGCAGGA GAGTCTCCAT GGACATTTGG ACAGGATACC
CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGGTTTGA TAATGACAGA AGTCTGCTCT CTAGAGGTA CTTGTAAACC TGTCCCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

FIG. 6A

801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GGCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTAGACCTTG AGAAGACAA CACACGGACG
126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CCGGTAACTC CCAGGAGAGT GTCACAGAGC AGACAGACAA
ACTTATTGAA GATAGGGTCT CTCGGGTTTC ATGTCACTT CCACCTATTG CCGGAGGTTA GCCATTGAG GGTCTCTCTCA CAGTGTCTCG TCCTGTCTGTT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GAGGCTGAGC AAAGCAGACT AGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTGGAGT CCGTCTGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CCGACGCTC AGTGGTAGT CCCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT AGCCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAAGC
AGCGGGCAGT GTTCTCTGAA GTTGTCCCT CTCACAAATTA ATTAGGAGA TGCGGCCTGC TGAGCACCGC TCGAGCCATG GGGCCCTAGA TCGGATTC
226 S P V T K S F N R G E C O

lambda t0 terminator^{*}

1201 CTCGGTTGCC GCCGGCGGTT TTTTATTGTT GCCGACGGC ATCTCGACTG CACGGTGAC CAATGCTTCT GCGGTCAGG AGCATCGGA AGCTGTGTA
GAGCCAACGG CCGCCCGCAA AAAATNACAA CCGCTGCGG TAGAGCTGAC GTGCCACGTG GTTACGAAGA CCGCAGTCCG TCGGTAGCCT TCGACACCAT

1301 TGGCTGTGCA GGTGCTAAAT CACTGCATAA TTCGTGTGCG TCAAGGGCA CTCCCGTTCT GGATAATGTT TTTTGGCGG ACATCATAC GGTCTTGCA
ACCGACAGT CCAGCATTA GTGACGTAAT AAGCACAGCG AGTTCGCGT GAGGGCAAGA CCTATTACAA AAAACGGCG TGTAGTATTG CCAAGACCGT

1401 AATATTCTGA AATGAGCTGT TGACAATTAA TCATCGAACT AGTTTAATGT GTGGAATTGT GAGCGGATAA CAATTAAAGT TAGGATCTAG AATTATGAAG
TTATAAGACT TTAATCGACA ACTGTTAAT AGTAGCTTGA TCAAAATTACA CACCTTAACA CTCGCCATT GTTAATTGA ATCTAGATC TTAATACTTC

M K
Start STII signal TIR 3^{*}

1501 AAGAAATTG CGTTCCTACT TGCTCTATG TTGTCTTTT CTATAGCTAC AAACGGTAC GCTGAGTTC AGCTGGTGA GTCTGGCGGT GGCCTGGTGC
TTCTTATAAC GCAAGGATGA ACGGAGATAC AAACAGAAAA GATATCGATG TTTGGCGATG CGACTCCAG TCGACCACT CAGACCGCCA CCGGACCAAG
3 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V Q

*anti-TF heavy chain

FIG. 6B

1601 AGCCAGGGG CTCACTCCGT TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGAGTACT ACATGCACTG GGTCCGTCAG GCCCGGGTA AGGGCCTGGA
TCGGTCCCC GAGTGAGGCA AACAGGACAC GTCGAAGACC GAAGTTATAA TTCTCATGA TGTACGTGAC CCAGGCAGTC CGGGGCCCAT TCCCGACCT
37 P G G S L R L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E

1701 ATGGGTTGA TTGATTGATC CAGAGCAAGG CAACAGATC TATGACCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA
TACCCAAACCT AACTAACTAG GTCTCGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCGGAC TGTTAAGTT TTTGTGTCGT
70 W V G L I D P E Q G N T I Y D P K F Q D R A T I S A D N S K N T A

1801 TACCTGCAGA TGAACAGCCT GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTGAGAC ACGGCGCTT ACTTCGACTA CTGGGTCAA GGAACCTGG
ATGGACGTCT ACTTGTCGGA CGCAGCACTC CTGTGACGGC AGATAATAAC ACAGCTCTG TSCGGCGGAA TGAAGCTGAT GACCCAGTT CTTGGGACC
103 Y L Q M N S L R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V

1901 TCACCGTCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GGTGCCTGGT
AGTGGCAGAG GAGCCGGAGG TGGTTCCCG GTAGCCAGAA GGGGACCGT GAGGAGGAGT TCTGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA
137 T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L V

^ApaI

2001 CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCC TCACCAGCG GGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC
GTTCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCCTGAG
170 K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L

2101 TACTCCCTCA GCAGCGTGGT GACTGTGCC TCTAGCAGCT TGGGCACCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA
ATGAGGGAGT CGTCGCACCA CTGACACGGG AGATCGTGA ACCCGTGGT CTGGATGTAG ACGTGCACT TAGTGTCCG GTCGTTGTTG TTCCACCTGT
203 Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K

2201 AGAAAGTTGA GCCCAAATCT TGTGACAAA CTCACACATG CCCACCGTC CCAGCACCTG AACTCCTGG GGGACCGTCA GTCTTCTCT TCCCCCAAA
TCTTCAACT CGGGTTTGA AACTGTTT GAGTGTGTAC GGGTGGCAG GGTGCTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGAGA AGGGGGTTT
237 K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P P K

FIG. 6C

2301 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGGCGTG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
TGGGTTCTTG TGGGAGTACT AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGTCT CTGGGACTCC AGTTCAAGTT GACCATGCAC
270 . P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V
2401 GACGGCGTGG AGGTGCATAA TGCCAAAGCA AAGCCGCGGG AGGAGCAGTA CAACAGCAGG TACCGTGTGG TCAGCGTCTCT CACCGTCTCTG CACCAGGACT
CTGCGGCACC TCCACGTATT ACGGTTCTGT TTGCGCGGCC TCCTCGTGCAT GTTGTGTGC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCTCTGA
303 D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W
2501 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GCCCCCATCG AGAAACCAT CTCCAAGCC AAAGGGCAGC CCCGAGAAAC
CCGACTTACC GTTCCTCATG TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CCGGGGTAGC TCTTTTGGTA GAGGTTTCGG TTTCGCTCGG GGGCTCTTGG
337 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P
2601 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGCTTCT ATCCAGCGA CATCGCCGTG
TGTCCACATG TGGACGGGG GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGACTG GACGACCAG TTTCGGAAGA TAGGTCGCT GTAGCGGCAC
370 Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V
2701 GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGTGGAC TCCGAGGGCT CCTTCTTCTCT CTACAGCAAG CTCACCGTGG
CTCACCTCT CGTTACCGT CGGCCTCTTG TTGATGTTCT GTGTGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTTG GAGTGGCACC
403 E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D
2801 ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCTG GAGGCTCTGC ACAACCACTA CAGCAGAGG AGGCTCTCCC TGTCCTCCGGG
TGTTCTCGTC CACCGTCGTC CCCTTGCGA AGAGTACGAG GCACTACGTA CTCGAGACG GTTGTGTGAT GTGGTCTTC TCGGAGAGGG ACAGAGGCC
437 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G
2901 TAAATAAGCA TGGCAGGCC CTAGAGTCCC TAACGCTCGG TTGCGCGCGG GCGTTTTTA TTGTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT
ATTATTCTGT ACCGTGCCGG GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAT AACAACTGT TACAACACTGT CGAATAGTAG CTATTTCGAAA
470 K O

FIG. 6D

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTATGTCTG TACTTTTATG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GGGCAAAATG ACCAACACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTCCG CAACTAACTA GTCCATCTCC

201 GGGCGCTGPA CGAGGTAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCAATA AGTGTCAAG GCCGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAATGTA TTTGTAACTA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAATAA AAANTTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAATA AGGGTATCTA GAATTATGAA AAAGAATATC GCATTTCCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGCTA CGCTGATATC
AGTGCATTTT TCCCATAGAT CTTAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^Start STII signal TIR 7 anti-tissue factor light chain^

501 CAGATGACCC AGTCCCGCAG CTCCTGTGCC GCCTCTGTGG GCGATAGGT CACCATACC TGCAGAGCCA GTCCGACAT CAAGAGCTAT CTGAACCTGGT
GTCTACTGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCA GTGGTAGTG AGTCTCGGT CAGCGTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTA CTATGTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GATACATGA TCAGAGCGAC TTCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAGAC TTCCGAACTT ATTACTGTCT TCAGCAGCGA GAGTCTCCAT GGACATTGG ACAGGGTACC
CTTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCTGCTC CTCAGAGGTA CCTGTAAACC TGTCCTCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

801 AAGGTGGAGA TCAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTTGC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTACACCTTG ACGAAGACAA CACACGGAGC

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

FIG. 7A

901 TGAATAACTT CTATCCCGA GAGGCCAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGTAACATC CCAGAGAGT GTACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGGTCT CTCGGTTTC ATGTACACTT CCACCTATTG CGGAGGTTA GCCCATTTAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K
1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACAGAGAAACA CAAAGTCTAC GCTGGGAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTCTGGAGT CGTCTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTCAGATG CGGAGGCTTC AGTGGGTAGT CCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S
1101 TCGCCCGTCA CAAAGAGCTT CAAAGGGGA GAGTGTAAAT TAAATCCTCT AGCGCGGAG CATCGTGGCG AGCTCGGTAC CCGGGATCT AGGCTAAGC
AGCGGGCAGT GTTCTCGAA GTTGTCCCT CTCACAATTA ATTAGGAGA TCGGGCCTGC GTAGCACCGC TCGAGCCATG GGCCCTAGA TCCGGATTGC
226 S P V T K S F N R G E C O
lambda t0 terminator^
1201 CTCGGTTGCC GCCGGCGGT TTTTATTGTT GCGGACGCG ATCTCGACTG CACGGTGCAC CAATGCTTCT GCGTCAAGC AGCCATCGGA AGCTGTGGTA
GAGCCAAACG CGGCCGCAA AAAATAACAA CCGCTGCGG TAGAGCTGAC GTGCCACGTG GTTACGAAGA CCGCAGTCCG TCGTAGCCT TCGACACCAT
1301 TGGCTGTGCA GGTCTGTAAT CACTGCATAA TTCGTGTGCG TCAAGGGCA CTCGCCGTTCT GGATAATGTT TTTTGGCCG ACATCATAC GGTCTCTGGCA
ACCGACACGT CCAGCATTA GTGACGTAAT AAGCACAGCG AGTCCGCGT GAGGGCAAGA CCTATTACAA AAAACGCGC TGTAGTATTG CCAAGACCGT
1401 AATATTCTGA AATGAGCTGT TGACAATTAA TCATCGAACT AGTTTAATGT GTGGAATGTT GAGCGGATAA CAATTAAGCT TAGGATCTAG AATTATGAAG
TTATAAGACT TTACTCGACA ACTGTTAAT AGTAGCTTGA TCAAAATTACA CACCTTAACA CTCGCCATT GTTAATTGA ATCTAGATC TTAATACITC
M K
Start STII signal TIR 3^
1
1501 AAGAATATTG CGTTCCTACT TGCCTCTATG TTTGTCTTTT CTATAGCTAC AAACGCGTAC GCTGAGGTTT AGCTGGTGA GTCTGGCGT GGCCTGGTC
TTCTTATAAC GCAAGGATGA ACGGAGATAC AACAGAGAAA GATATCGATG TTTGGCGATG CGACTCCAAG TCGACCACT CAGACCGCCA CCGGACCACG
3 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V Q
anti-tissue factor heavy chain with cys to ser in hinge^
1601 AGCCAGGGG CTCACCTCGT TTGTCTCTGG CAGCTTCTGG CTTCATATT AAGGAGTACT ACATGCACTG GGTCCGTGAG GCCCGGGTA AGGCTCTGGA
TCGGTCCCC GAGTGAGCA AACAGGACAC GTCGAAGACC GAAGTTATPA TTTCTCATGA TGTACGTGAC CCAGGCACT CCGGGCCCAT TCCCGGACCT
37 P G G S L R L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E

FIG. 7B

1701 ATGGGTTGGA TTGATTGATC CAGAGCAAGG CAACACGATC TATGACCGA AGTTCAGGA CCGTGCCACT ATAAGGCTG ACAATTCCAA AAACACAGCA
TACCCAACT AACTAACTAG GTCTCGTTCC GTTGCTGTAG ATACTGGCT TCAAGGTCTT GGCACGGTGA TATTCGGAC TGTTAAGTT TTTGTGTCGT
70 W V G L I D P E Q G N T I Y D P K F Q D R A T I S A D N S K N T A

1801 TACCTGCAGA TGAACAGCCT GCGTGTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCGCTT ACTTCGACTA CTGGGTCAA GGAACCCCTGG
ATGGACGTCT ACTGTGCGA CGCAGACTC CTGTGACGGC AGAATAAAC ACGAGTCTG TGCCGGCGAA TGAAGCTGAT GACCCAGTT CTTTGGGACC
103 Y L Q M N S L R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V

1901 TCACCGTCTC CTGGGCTCC ACCAAGGCC CATGGTCTT CCCCTGGCA CCTCTCTCA AGACACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT
AGTGGCAGAG GAGCCGGAGG TGGTCCCGG GTAGCCAGAA GGGGACCGT GAGAGGAGT TCTGTGGAG ACCCCGCTG CGCGGGACC CGACGGACCA
137 T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L V

2001 CAAGGACTAC TTCCCGAAC CCGTGACGGT GTCTGGAAC TCAGGGCCC TGACCAGCG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC
GTTCTGATG AAGGGCTTG GCCACTGCCA CAGCACTTG AGTCCGGGG ACTGGTCGCC GCAGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCTGAG
170 K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L

2101 TACTCCCTCA GCAGCGTGGT GACTGTGCC TCTAGCAGCT TGGGCACCA GACCTACATC TGCAACGTGA ATCAACAGCC CAGCAACACC AAGTGGACA
ATGAGGGAGT CGTGCACCA CTGACACGG AGATCGTGA ACCCGTGGT CTGGATGTAG ACGTTGCAC TAGTGTTCGG GTCGTTGTTG TTCCACCTGT
203 Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K

2201 AGAAAGTTGA GCGCAATCT TGTGACAAA CTCACACTAG TCCACCGTCT CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTCTCTCT TCCCCCAA
TCTTTCACT CGGGTTTGA AACTGTTT GAGTGTGATC AGGTGGCAGA GGTGTTGAC TTGAGGACCC CCTGGCAGT CAGAAGGAGA AGGGGGGTTT
237 K V E P K S C D K T H T S P P S P A P E L L G G P S V F L F P P K
^Hinge cys to ser ^Hinge cys to ser

2301 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCCCTGAG TCAAGTTCAA CTGGTACGTG
TGGGTTCTG TGGGAGTACT AGAGGGCCTG GGGACTCCAG TGTAGGCACC ACCACCTGCA CTCGGTGCCT CTGGGACTCC AGTTCAAGTT GACCATGCAC
270 P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V

FIG. 7C

2401 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGGCGG AGGAGCAGTA CAACAGCAGG TACCGTGTGG TCAGCGTCTT CACCGTCTCG CACCAGGACT
CTGCCGCACC TCCACGATTT ACGGTTCTCT TTCCGGCGCC TCCTCGTCAT GTTGTCGTC AGTCGACACC ATGCGCAGGA GTGCGAGGAC GTGGTCTCTGA
303 D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W

2501 GGCTGAATGG CAAGGAGTAC AAGTGCAGG TCTCCACAAA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAGCC AAAGGGCAGC CCGAGAACC
CCGACTTACC GTTCTCATG TTCACGTTCC AGAGTTGTT TCGGGAGGGT CCGGGGTAGC TCTTTTGTA GAGGTTTGG TTTCCCGTCG GGGCTCTTGG
337 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P

2601 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGTC AAAGGTTCT ATCCACGGA CATCGCCGTC
TGTCACATG TGGGACGGGG GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGACTG GACGGACCAG TTTCCGAAGA TAGGTCGCT GTAGCGGCAC
370 Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V

2701 GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGTGGAC TCCGAGGGCT CCTTCTTCT CTACAGCAAG CTCACCGTGG
CTCACCTCT CGTTACCCGT CGGCCTCTTG TTGATGTTCT GGTGGGAGG GCACGACCTG AGGCTGCCA GGAAGAAGGA GATGCTGTT CAGTGGCACC
403 E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D

2801 ACAAGAGCAG GTGGCAGCAG GGGAAAGTCT TCTCATGCTC CGTATGCTC GAGGCTCTGC ACAACACTA CACGAGAAG AGCTCTCCC TGCTCCGGG
TGTTCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCGAGACG TGTTGGTGAT GTGGTCTTC TCGAGAGGG ACAGAGGCC
437 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G

2901 TAAATAAGCA TGGACGGCC CTAGAGTCCC TAAGCTCGG TTGCGCGCGG GCGTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT
ATTTATTCGT ACGCTGCCGG GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAACTGT TACAATGAG CGAATAGTAG CTATTGAAA
470 K O

FIG. 7D

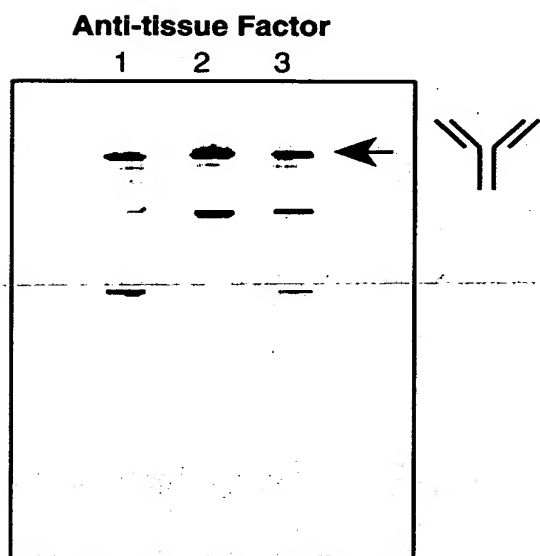


FIG. 8A

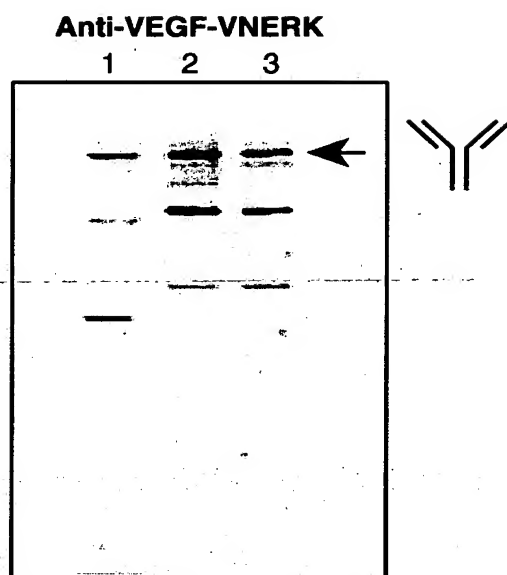


FIG. 8B

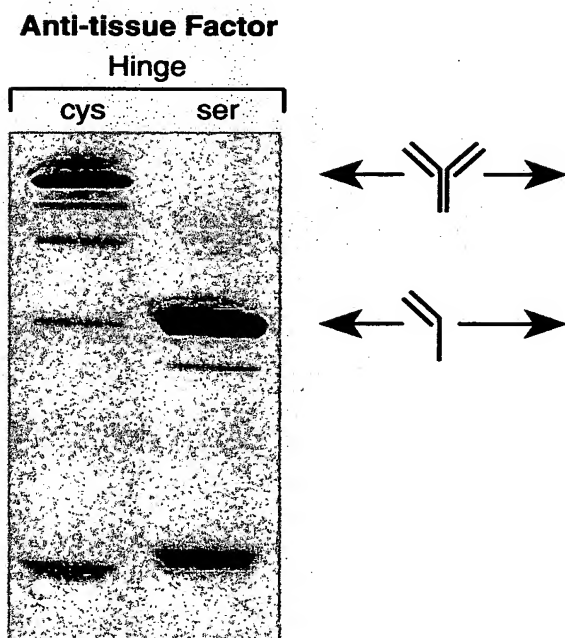
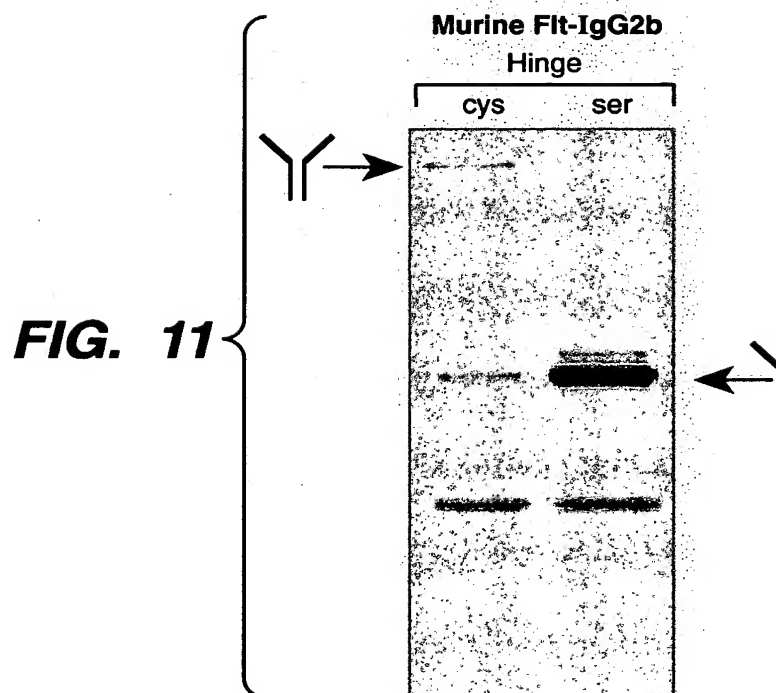
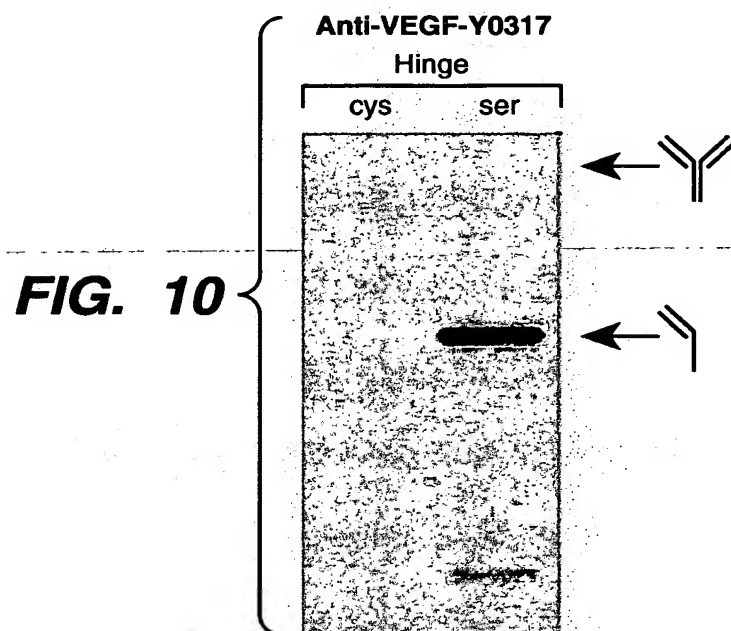


FIG. 9A



FIG. 9B



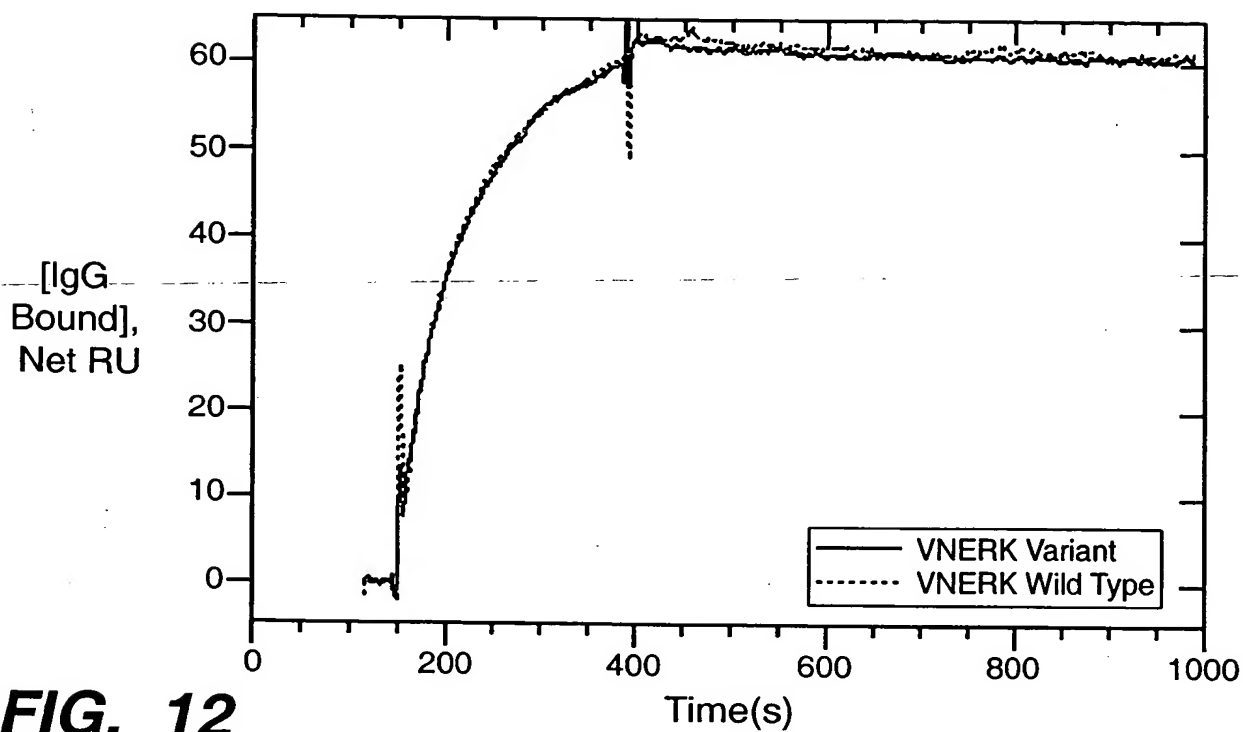


FIG. 12

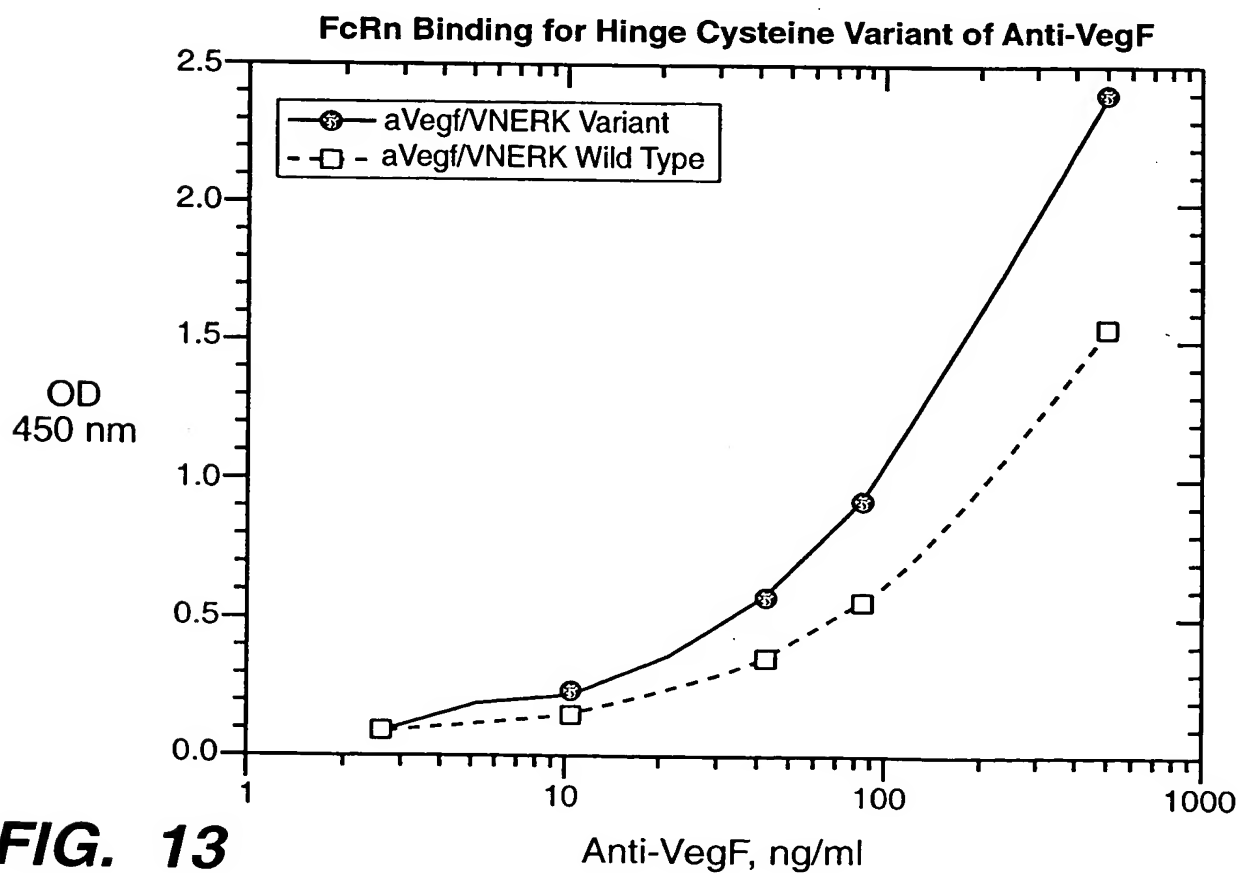


FIG. 13

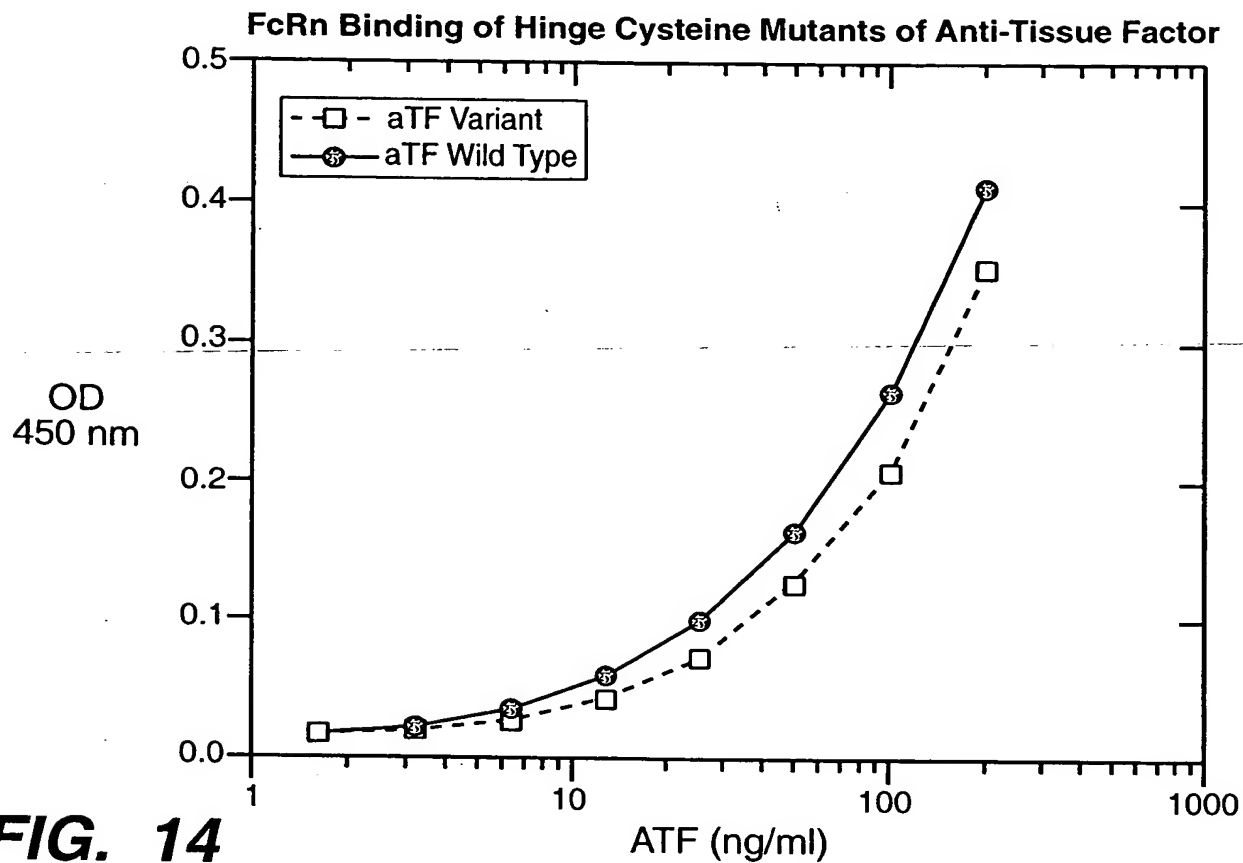


FIG. 14

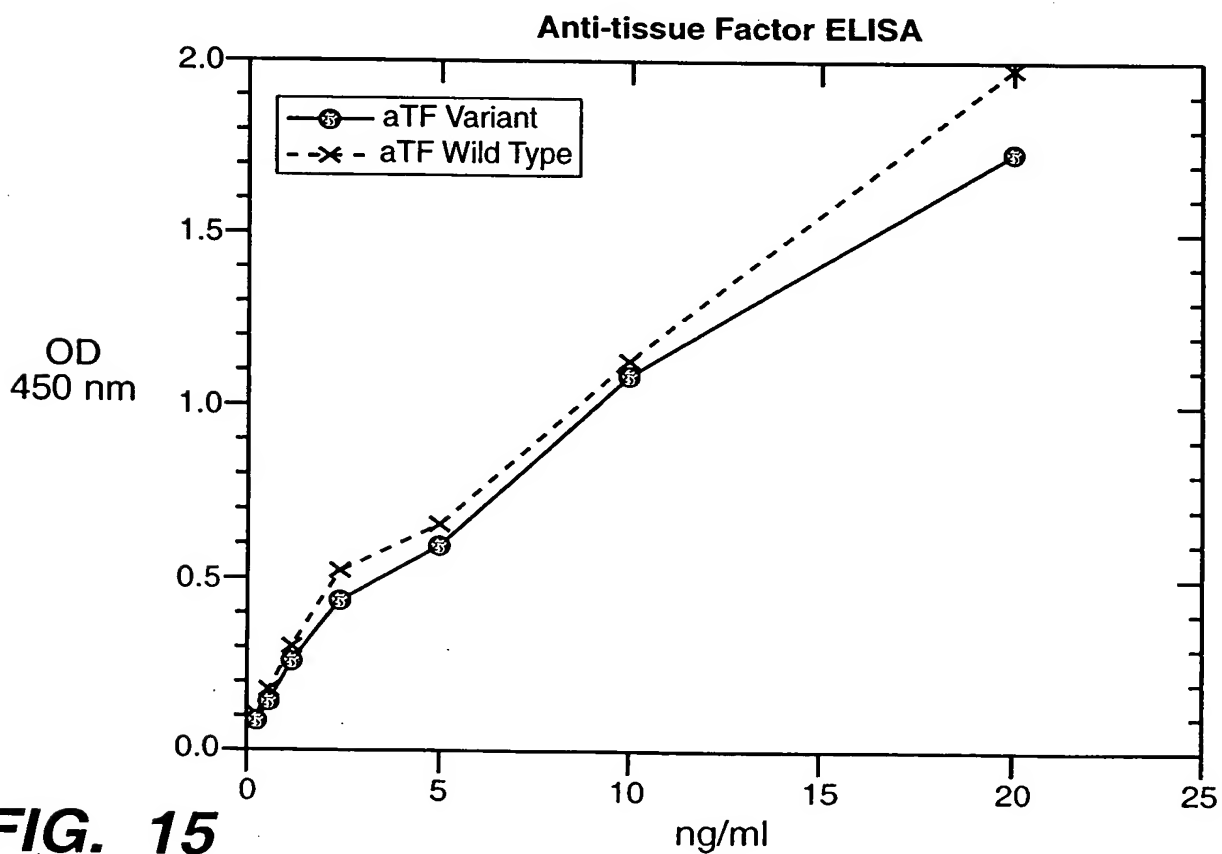
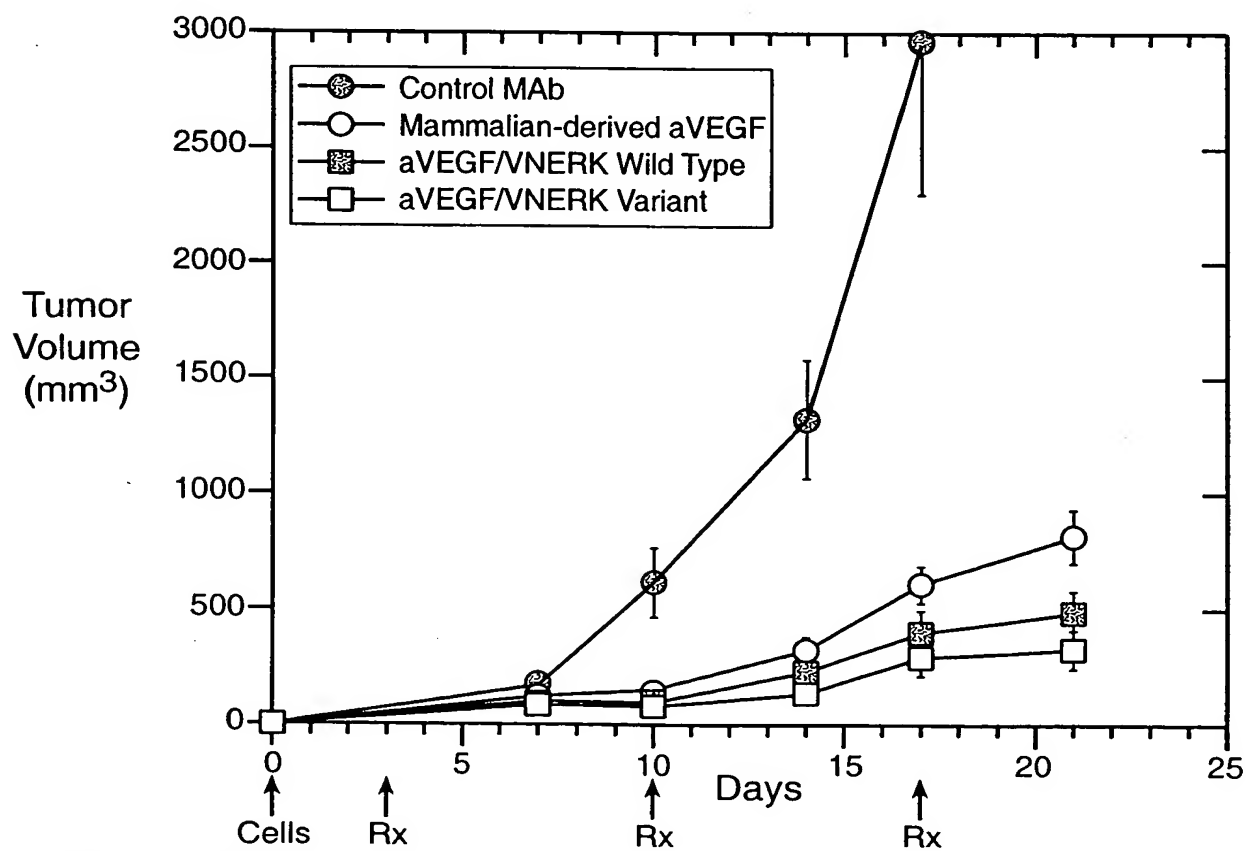
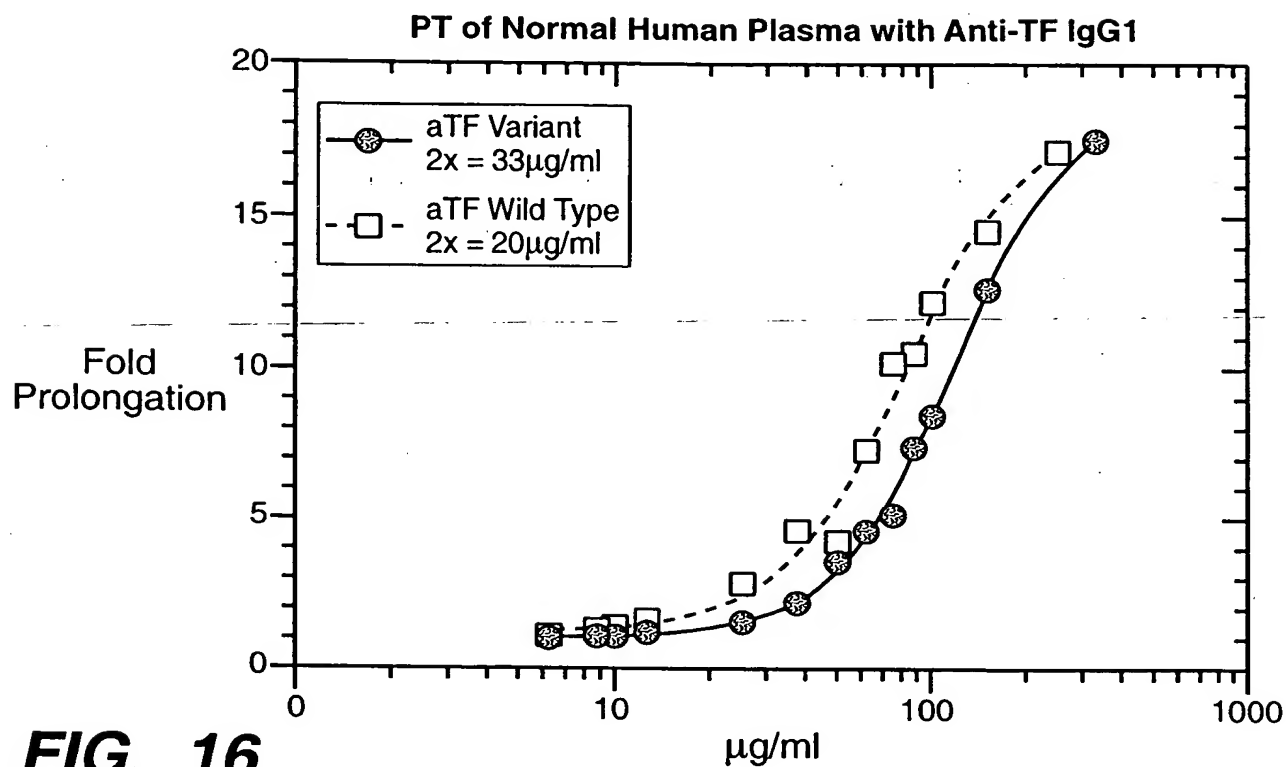


FIG. 15



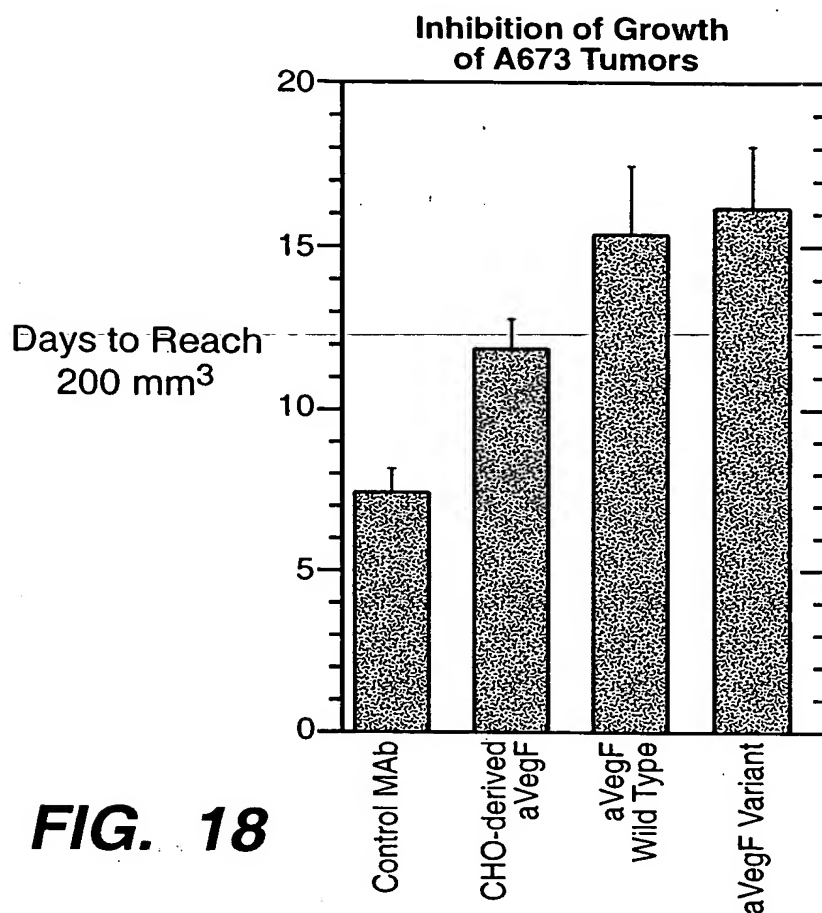


FIG. 18

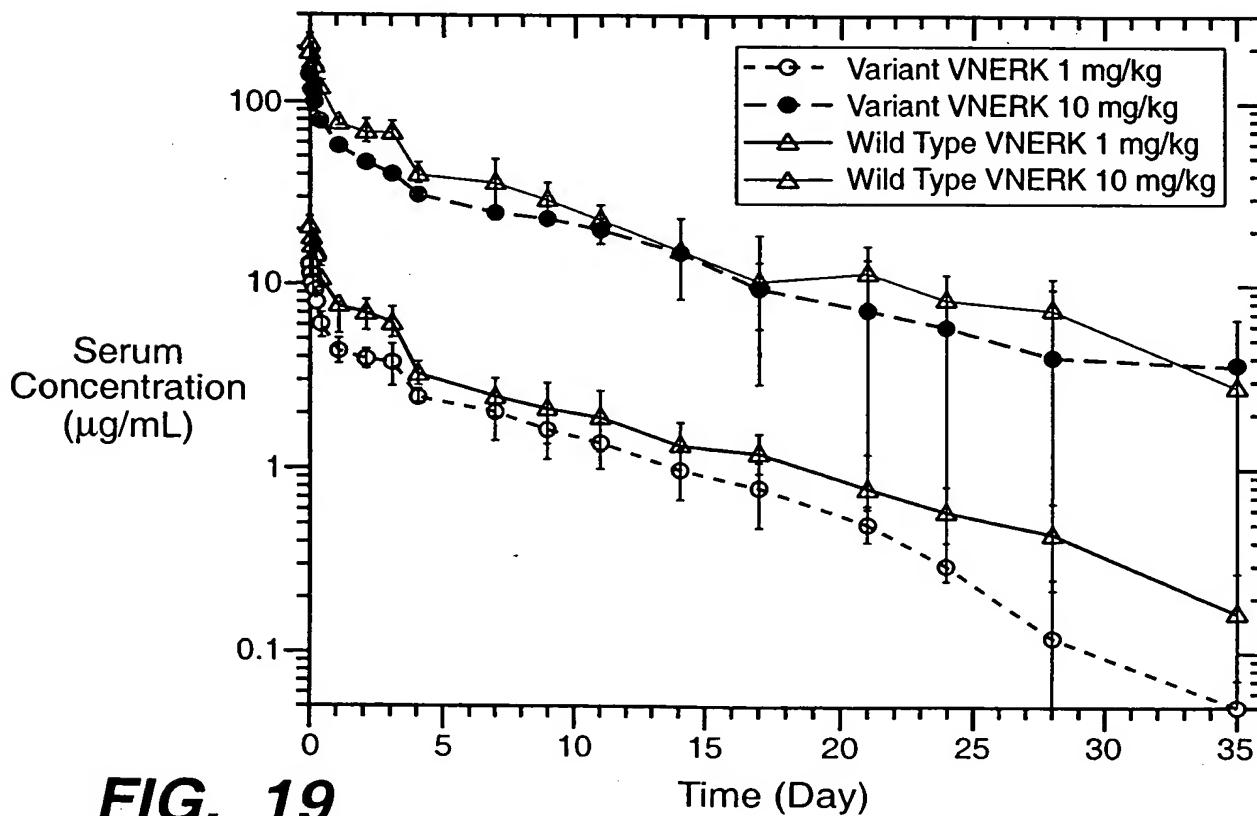


FIG. 19